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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/609,078	06/27/2003	Edmund H. Crane III	035718/262707(5718-197A)	2573

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EXAMINER

KUBELIK, ANNE R

ART UNIT PAPER NUMBER

1638

DATE MAILED: 05/12/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.		Applicant(s)	
	10/609,078		CRANE, EDMUND H.	
	Examiner		Art Unit	
	Anne R. Kubelik		1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☐ Responsive to communication(s) filed on _____.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-17 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-17 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>search results</u> . |

DETAILED ACTION

1. Claims 1-17 are pending
2. In the IDS filed 27 June 2003 the BLAST alignment results have been crossed out, as these are not published literature. The information therein has been considered, however.

Claim Objections

3. Claims 1, 8-9 and 13 are objected to because of the following informalities:

Claim 1, part (g), has an improper article before the second "polynucleotide".

Claim 8 misspells "from".

Claims 9 and 13 have an improper article before "Rar-1" in part (a).

Claim Rejections - 35 USC § 112

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

5. Claims 1-17 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claims contain subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claims are broadly drawn to nucleic acids that encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO: 2, 3, 7 or 9 under "high stringency conditions", that would be amplified from a maize nucleic acid library using primers that selectively hybridize

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under high stringency conditions to loci within SEQ ID NO: 2, 3, 7 or 9, that have 85% identity to SEQ ID NO:2, 3, 7 or 9, or that encode a protein with 85% identity to SEQ ID NO:8. The claims are also drawn to vectors and expression cassettes comprising the nucleic acids, cells and plants comprising the expression cassettes and methods of using the expression cassettes to modulate the level of Rar1-interactor protein in a plant and to enhance diseased resistance in a plant.

The instant specification, however, only provides guidance for yeast-two hybrid analysis to find maize nucleic acids encoding proteins that interact with the Rar1 protein (example 1), isolation of full-length cDNAs encoding the proteins (example 2); a BLAST comparison of the sequences of the nucleic acids (example 3); general guidance for transformation of maize, soybean and sunflower (examples 4-7). SEQ ID NO:1 encodes a protein that has homology to wheat heat-shock protein 80; SEQ ID NOs 2 and 3 are fragments of SEQ ID NO:7, which encodes a protein, SEQ ID NO:8, that has homology to rice SGT1; SEQ ID NO:9 is the coding sequence for that protein (pg 57).

The specification does not teach where to find or how to make nucleic acids that encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO: 2, 3, 7 or 9 under “high stringency conditions”, that would be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO: 2, 3, 7 or 9, that have 85% identity to SEQ ID NO:2, 3, 7 or 9, or that encode a protein with 85% identity to SEQ ID NO:8.

Making substitutions in proteins does not produce predictable results. Hill et al (1998, Biochem. Biophys. Res. Comm. 244:573-577) teach that when three histidines that are

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maintained in ADP-glucose pyrophosphorylase across several species are substituted with the “nonconservative” amino acid glutamine, there is little effect on enzyme activity, while the substitution of one of those histidines with the “conservative” amino acid arginine drastically reduced enzyme activity (see Table 1).

Given the claim breath, unpredictability, and lack of guidance as discussed above, undue experimentation would have been required by one skilled in the art to develop and evaluate nucleic acids encoding proteins with 85% identity to SEQ ID NO:8. Making all possible single amino acid substitutions in an 361 protein like that of SEQ ID NO:8 would require making and analyzing 19^{361} nucleic acids; these proteins would have 99.7% identity to SEQ ID NO:8. Because nucleic acids encoding proteins with 85% identity to SEQ ID NO:1 would have 54 nucleotide substitutions, many more than 3^{691} nucleic acids would need to be made and analyzed. Guo et al. (2004, Proc. Natl. Acad. Sci. USA 101: 9205-9210) teach that while proteins are fairly tolerant to mutations resulting in single amino acid changes, increasing the number of substitutions additively increases the probability that the protein will be inactivated (pg 9209, right column, paragraph 2). Thus, making and analyzing proteins with 54 amino acid substitutions that also have Rar-1 interactor activity would require undue experimentation.

The specification does not teach how to use nucleic acids that encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO: 2, 3, 7 or 9 under “high stringency conditions”, that would be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO: 2, 3, 7 or 9, that have 85% identity to SEQ ID NO:2, 3, 7 or 9, or that encode a protein with 85% identity to SEQ ID NO:8.

The specification teaches that the invention is a method of modulating the level of a protein and enhancing disease resistance in a plant by transformation with a nucleic acid of the invention (pg 3, lines 8-12; pg 4, lines 11-20); and that modulating the level of the protein can be accomplished by up or down regulation of the gene (pg 45, line 26, to pg 47, line 2). the specification does not teach which method, up-regulation or down-regulation will enhance disease resistance in a plant, and thus does not teach how to use the instant nucleic acid.

In *N. benthamiana* suppression of SGT1 resulted in plants that have lost resistance to tobacco rattle virus (Liu et al, July 2002, Plant Cell 14:1483-1496, see pg 1488, right column paragraph 4), and silencing of the barley SGT1 gene resulted in the reduction of R-gene-dependent disease resistance (Azevedo et al, pg 2075, column 3, paragraph 3). Thus, the claimed nucleic acid cannot be used in an antisense manner to enhance disease resistance in a plant, and SEQ ID NO:2 and 3, which are only partial sequences and can only be used in an antisense method cannot be used enhance disease resistance in a plant. Furthermore, a method of reducing the level of SGT1 protein in a plant has no use, given that plants without disease resistance have no utility.

The protein of SEQ ID NO:8 has 61.7% similarity to *Arabidopsis* SGT1a and 61.0% similarity to SGT1b (see sequence search results); it is not clear to which, if either, SEQ ID NO:8 is functionally equivalent. Austin et al (March, 2002, Science 295:2077-2080) teach that AtSGT1b is essential for resistance, while AtSGT1a is not (pg 2078, column 1, paragraphs 2-3), even though both interact with RAR1 in a yeast two-hybrid assay (Azevedo et al, March 2002, Science 295:2073-2076; see pg 2074, column 1, paragraph 3). AtSGT1a was also unable to

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complement *Nicotinana benthamiana* SGT1, while AtSGT1b was able to do so (Liu et al, pg 1490, right column, paragraph 2).

Plant SGT1 interacts with RAR1, SKP1 and HSP90 and all three of these proteins are involved in conferring disease resistance (Takahashi et al, 2003, Proc. Natl. Acad. Sci. USA 100:11777-11782, see pg 11781, left column, paragraph 2; Liu et al).

Thus, it is not clear that transformation of a plant with a nucleic acid encoding SEQ ID NO:8 will enhance disease resistance in a plant.

As the specification does not describe the transformation of any plant with SEQ ID NO:1 or nucleic acids that both interact with Rar1 and encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO:1 under “high stringency conditions”, that would be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO:1, or that have 80% identity to SEQ ID NO:1, undue trial and error experimentation would be required to screen through the myriad of nucleic acids encompassed by the claims and plants transformed therewith, to identify those with modulated Rar-1 interactor protein or enhanced disease resistance, if such plants are even obtainable.

Given the claim breath, unpredictability in the art, undue experimentation, and lack of guidance in the specification as discussed above, the instant invention is not enabled throughout the full scope of the claims.

6. Claims 1-15 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter that was not described

in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are broadly drawn to a multitude of nucleic acids that interact with Rar1, that both interact with Rar1 and encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO:1 under “high stringency conditions”, that would be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO:1, or that have 80% identity to SEQ ID NO:1. No such nucleic acid is described in the specification.

The specification does describe SEQ ID NO:1, but it does not interact with Rar1. The specification does not describe the structural features of any nucleic acids that can be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO:1, nor are the primers or loci described.

If it is not the nucleic acid that interacts with Rar1, but the protein, claim 1, parts (a) and (c)-(e) do not recite the function of the protein encoded by the nucleic acid.

A wide range of proteins can interact with Rar1 at some point in the cell, including proteins involved in translation and degradation. The specification does not describe maize nucleic acids encoding such proteins within the full scope of the claims.

Hence, Applicant has not, in fact, described DNA molecules that interact with Rar1 or for nucleic acids that both interact with Rar1 and encode a maize protein that interacts with Rar1, and the specification fails to provide an adequate written description of the claimed invention.

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Therefore, given the lack of written description in the specification with regard to the structural and physical characteristics of the claimed compositions, it is not clear that Applicant was in possession of the genus claimed at the time this application was filed.

See *Univ. of California v. Eli Lilly*, 119 F.3d 1559, 43 USPQ 2d 1398 (Fed. Cir. 1997):

The name cDNA is not in itself a written description of that DNA; it conveys no distinguishing information concerning its identity. While the example provides a process for obtaining human insulin-encoding cDNA, there is no further information in the patent pertaining to that cDNA's relevant structural or physical characteristics; in other words, it thus does not describe human insulin cDNA Accordingly, the specification does not provide a written description of the invention

and at pg 1406:

a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA," without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicted, does not suffice to define the genus because it is only an indication of what the genes does, not what it is.

... A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus.

... the claimed genera of vertebrate and mammal cDNA are not described by the general language of the '525 patent's written description supported only by the specific nucleotide sequence of rat insulin.

See *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ 2d 1016 at page 1021:

A gene is a chemical compound, albeit a complex one, and ... conception of a chemical compound requires that the inventor be able to define it so as to distinguish it from other materials Conception does not occur unless one has a mental picture of the structure of the chemical or is able to define it by its method of preparation, its physical or chemical properties, or whatever characteristics sufficiently distinguish it. It is not sufficient to define it solely by its principal biological property, *e.g.*, encoding human erythropoietin, because an alleged conception having no more specificity than that is simply a wish to know the identity of any material with that biological property.

7. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

8. Claims 1-15 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention. Dependent claims are included in all rejections.

Claim 1 is indefinite in its recitation of both “an isolated nucleic acid capable of interacting with Rar1” in line 1 and “a polynucleotide encoding a maize Rar-1 interactor protein” in part (b). Is it the protein or the nucleic acid that interacts with Rar-1? Or does the nucleic acid both interact with Rar-1 AND encode a protein that also interacts with Rar-1 (part (b))? Furthermore, what is the nature of that interaction? Is an Rar-1 interactor a protein that only binds to Rar-1 or is it a protein that interacts with Rar-1 in any way (and thus including proteins like translation and degradation proteins. Similarly, in claims 9 and 13, it is not clear which, the protein, the nucleic acid or both, is the Rar-1 interactor.

Claim 1 is indefinite in its recitation of “selectively hybridize” in part (a). It is not clear what extent of hybridization is considered “selective”; thus, the metes and bounds of the claimed nucleic acid are unclear.

Claim 1 is indefinite in its recitation of “high stringency conditions” in parts (a) and (e). It is not clear what hybridization conditions are considered “high stringency”. The term is a relative term that is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the metes and bounds of the invention.

Claim 3 lacks antecedent basis for the limitation “member of claim 1” as claim 1 is drawn to an isolated nucleic acid.

Claims 7, 10 and 14 are indefinite because a plant cannot be a maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet plant.

It is unclear if the seed of claim 8 comprises the recombinant expression cassette of claim 3 or if the seed is transgenic because it was transformed with another nucleic acid. Not all seeds from a transgenic plant will comprise the nucleic acid with which the plant was transformed.

Claims 9 and 13 lack antecedent basis for the limitation “Rar-1 interactor polynucleotide of claim 1” in part (a), as claim 1 is drawn to a nucleic acid.

In claims 9 and 13, parts (b), it is not clear if “plant growing conditions” would regenerate a plant from a plant cell, because the conditions required to grow a plant are different from the ones required to regenerate one. It is suggested that part (b) be replaced with --(b) regenerating a plant from the plant cell--.

In claims 9 and 13, parts (c), it is not clear what action the practitioner takes to induce expression of the polynucleotide. The promoter operably linked to it in part (a) is not an inducible promoter, which can be “induced” by the practitioner.

In claims 9 and 13, parts (c), it is not clear what it means to “modulate Rar1-interactor protein”. What is being done to it? What is being “modulated”? The protein activity? The level of the protein? Furthermore, claim 13 is drawn to a method of enhancing disease resistance in a plant, not to a method of modulating Rar-1-interactor protein.

Claim Rejections - 35 USC § 102

9. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

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(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

10. SEQ ID NO:2 corresponds to bases 1-571 of SEQ ID NO:7 and SEQ ID NO:3 corresponds to bases 1042-1430 of SEQ ID NO:7. SEQ ID NOs:2 and 3 are present in parent application 10/074,473, filed 12 February 2002; SEQ ID NOs:7-9 are not. Thus, the effective filing date for SEQ ID NOs:7-9 is the filing date of the instant application, 27 June 2003.

11. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(a) as being anticipated by Hainey et al (October, 2002, GenBank Accession No. AY103953).

Hainey et al teach an isolated maize nucleic acid that has 98.7% identity to bases 24-1430 of SEQ ID NO:7 and 99.0% identity to bases 1-1086 of SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

12. Claims 1 and 16-17 are rejected under 35 U.S.C. 102(a) as being anticipated by Lai et al (2002, GenBank Accession No. CA401716).

Lai et al teach an isolated maize nucleic acid that has 99.3% identity to SEQ ID NO:7 (see sequence search results). It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

13. Claims 1 and 16-17 are rejected under 35 U.S.C. 102(a) as being anticipated by Lai et al (3 June 2003 GenBank Accession No. CD443320).

Lai et al teach an isolated maize nucleic acid with 99.6% identity to bases 24-736 of SEQ ID NO:7 and 99.5% identity to bases 1-655 of SEQ ID NO:9 (see sequence search results). It

would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

14. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW076372).

Walbot et al teach an isolated maize nucleic acid that has 99.8% identity to bases 735-1366 of SEQ ID NO:7 and 99.8% identity to bases 397-1050 of SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

15. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW090936).

Walbot et al teach an isolated maize nucleic acid that has 99.8% identity to bases 121-965 of SEQ ID NO:7 and 99.8% identity to bases 240-884 of SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

16. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW076374).

Walbot et al teach an isolated maize nucleic acid that has 99.7% identity to bases 478-1131 of SEQ ID NO:7 and 99.8% identity to SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to

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SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

17. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW155786).

Walbot et al teach an isolated maize nucleic acid that has 100.0% identity to bases 829-1455 of SEQ ID NO:7 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

18. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW042392).

Walbot et al teach an isolated maize nucleic acid that has 99.8% identity to SEQ ID NO:7 and 99.7% identity to bases 147-732 of SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

19. Claims 1-6, 9, 11, 13 and 16-17 are rejected under 35 U.S.C. 102(a and e) as being anticipated by Liu et al, US2004/0034888A1, filed April 2003.

Liu et al teach isolated nucleic acids with 99.4%, 94.1%, 86.6% and 92.3% identity to SEQ ID NO:7 and 99.9%, 94.1%, and 99.4% identity to SEQ ID NO:9; the nucleic acids encode proteins with 100%, 93.5% and 93.1% identity to amino acids 1-361 of SEQ ID NO:8 (see sequence search results). They would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

Liu et al also teach recombinant DNA constructs comprising the nucleic acids and methods of using them to increase resistance to plant disease (claims 1-3).

20. Claims 1-6, 8-9, 11, 13 and 16-17 are rejected under 35 U.S.C. 102(a and e) as being anticipated by La Rosa et al, US2004/0214272, filed April 2003.

La Rosa et al teach isolated nucleic acids with 98.6% and 92.3% identity to SEQ ID NO:7 and 99.9%, 94.1% and 86.6% identity to SEQ ID NO:9 (see sequence search results). They would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9. La Rosa et al also teach recombinant DNA constructs comprising the nucleic acids and methods of using them to increase resistance to plant disease (claims 1-3).

21. Claims 1-6, 8-9, 11 and 13 are rejected under 35 U.S.C. 102(b) as being anticipated by Liu et al, July 2002, Plant Cell 14:1483-1496).

Liu et al teach isolated nucleic acids that would hybridize to SEQ ID NO:7 and 9 because they have regions of high identity (see sequence search results). Liu et al also teach tobacco plants transformed with the nucleic acids (pg 1490, right column, paragraphs 1-2).

22. Claims 12 and 15 are free of the prior art, given the failure of the prior art to teach or suggest a method of enhancing disease resistance or altering the level of an Rar1-interactor protein by transformation with a nucleic acid of SEQ ID NO:2, 3, 7 or 9. Claims 7, 10 and 14 are free of the prior art, given the failure of the prior art to teach or suggest plants that are maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet.

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Conclusion

23. No claim is allowed.

24. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne R. Kubelik, whose telephone number is (571) 272-0801. The examiner can normally be reached Monday through Friday, 8:30 am - 5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson, can be reached at (571) 272-0804. The central fax number for official correspondence is (571) 273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

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For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

Anne R. Kubelik, Ph.D.
May 6, 2005



**ANNE KUBELIK, PH.D.
PRIMARY EXAMINER**


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Db 125 LTFVPUKAEADGAARSVASFVEEKDAAANMDNTPPMVE--VRPKYRHDFFYNSATEVLT 182
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QY 357 KKWEY 361
Db 363 KKWEY 367

RESULT 4
Q84UV7
ID Q84UV7 PRELIMINARY; PRT; 370 AA.
AC Q84UV7;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE SGT1a.
OS Nicotiana benthamiana.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4100;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22115173; PubMed=12119369;
RA Liu Y., Schiff M., Serino G., Deng X.W., Dinesh-Kumar S.P.;
RT "Role of SCF ubiquitin-ligase and the COP9 signalosome in the N gene-
RL mediated resistance response to Tobacco mosaic virus.";
DR Plant Cell 14:1483-1496(2002).
DR EMBL; AF494083; AA085509.1; -.
DR InterPro; IPR007052; CS;
DR InterPro; IPR008978; HSP20_chap.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF04969; CS; 1.
DR Pfam; PF00515; TPR 1; 1.
DR SMART; SM00028; TPR 3.
DR PROSITE; PS50005; TPR; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Repeat; TPR repeat.
SQ SEQUENCE 370 AA; 41240 MW; 88EF4C3408F5121P CRC64;

Query Match 66.8%; Score 1243; DB 2; Length 370;
Best Local Similarity 66.2%; Pred. No. 7.5e-73;
Matches 245; Conservative 48; Mismatches 63; Indels 14; Gaps 5;

QY 3 ASDLESKAKAEAFVDDDFELATELYSQDAIDAGPATADLYADRAQAHIKLGNYTEAVDANK 62
Db 2 ASDLETRAKAEAFDDHDELAVDLTQALMTPKNAELFADRAQAQNTKLTFTTEAVDANK 61
QY 63 AIELDPMMHKAYVRKGAACIKLEEYOTAKAALGSSYASGDSRPARLLKCEDERIAEES 122
Db 62 AIELDPMSKAYLRKGLAKMKLEEYOTAKAALGTASLAPAESRFTKLIKCEDERIAEEA 121
QY 123 SQAPVKNVEATVAATIED--KEFTNMENTPPVIEP-----PSKPKYRHDYNSAT 171
Db 122 GELNPNSVDKTSNGNVAPPASESLDNVAVAPKDAQPTVNLISYQCSAARPKYRHEFYQKPE 181
QY 172 EVLITFAKGVADSVVDVDFGEQMLSVSIEVPGEPYHFQPRFLFSKIIPKCKYQVLTSTK 231
Db 182 EVVVTIFAKGIPAKNVVVDVDFGEQMLSVSIEVDVGDGTYSFQPRFLGKITPAKCRFYMSTK 241
QY 232 VEIRLAKAEQVTTWTLDSGRPKTVPOKISTPAETAPRPSYPSSKAKK--DWDKLEAEVKK 290

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Db 242 IEIRLAKAEPLHTSWTLEVT--RASVVQRPNNVSSD--APRPSYSSKLURHVDWDKLEAEVKK 299
QY 291 EPKEEKLGDGAALNKFRRDIYKDADEDMRRAMKSFVESNGTGLSTNNKWDGAKKVEGSP 350
Db 300 ESKDEKLGDGAALNKFRRDIYKDADEDMRRAMKSFVESNGTGLSTNNKWDGAKKVEGSP 359
QY 351 PDGMELKKWE 360
Db 360 PDGMELKKWE 369

RESULT 5
Q8WS15
ID Q8WS15 PRELIMINARY; PRT; 350 AA.
AC Q8WS15;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE SGT1a.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi9.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21893744; PubMed=11847307; DOI=10.1126/science.1067554;
RA Azevedo C., Sadanandom A., Kitagawa K., Fraaijdenhoven A., Shirasu K.,
RA Schulze-lefert P.;
RT "The RAR1 interactor SGT1, an essential component of R gene-triggered
RT disease resistance.";
RL Science 295:2073-2076(2002).
DR EMBL; AF439975; AAL33611.1; -.
DR HSP; P31948; 1ELW.
DR Pfam; PF04969; CS; 1.
DR Pfam; PF05002; SGS; 1.
DR Pfam; PF00515; TPR 1; 2.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS50005; TPR; 2.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Repeat; TPR repeat.
SQ SEQUENCE 350 AA; 39277 MW; D23DBE990C817FB4 CRC64;

Query Match 61.4%; Score 1142; DB 2; Length 350;
Best Local Similarity 61.7%; Pred. No. 2.6e-66;
Matches 222; Conservative 56; Mismatches 68; Indels 14; Gaps 4;

QY 3 ASDLESKAKAEAFVDDDFELATELYSQDAIDAGPATADLYADRAQAHIKLGNYTEAVDANK 62
Db 2 AKELADKAKAEAFVDDDFDVAVDLYSKAIDLDPNCABFFADRAQAQYIKLESFTEAVDANK 61
QY 63 AIELDPMMHKAYVRKGAACIKLEEYOTAKAALGSSYASGDSRPARLLKCEDERIAEES 122
Db 62 AIELDPSLTAKYLRKGTACMKLEEYRTAKTALSKASITPESKFKKLIIDECNFLTIEE 121
QY 123 SQAPVKNVEATVAATIEDKEDFTNMENTPPVIEPSPK--KYRHDYNSATEVLTIFAK 180
Db 122 KDL-VQPVSTLPSSV-----TAPVSELDVTPTAKYRHEFYQKEVEVVVTFK 170
QY 181 GVPADSVVDFGEQMLSVSIEVPGEPYHFQPRFLFSKIIPKCKYQVLTSTKVEIRLAKAE 240
Db 171 GIPKQNVNDFGEQILSVSIEVPGEDAYVLPRLFGKIIPDKCKYEVLTSTKIEIRLAKAD 230
QY 241 QVTTWTLDSGRPKTVPOKISTPAETAPRPSYPSSKAKKWDKLEAEVKKKEEKLDGD 300
Db 231 IITWASLEHGKGPVLP--KPNVSSEVSQRPAYSPSSKKVWDKLEAEVKKQKDEKLEG 289
QY 301 AALNKFRRDIYKDADEDMRRAMKSFVESNGTGLSTNNKWDGAKKVEGSPDGMELKKWE 360
Db 290 AALNKFREIYQNADEDMRRAMKSFVESNGTGLSTNNKWDGAKKVEGSPDGMELKKWE 349

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At 56T1A

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 20, 2005, 18:18:25 ; Search time 40 seconds
(without alignments)
868.356 Million cell updates/sec

Title: US-10-609-078-8
Perfect score: 1861
Sequence: 1 MAASLESKAKEAFVDDDFE.....GAKKVEGPPDGMELKKWEY 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl2: *
3: Pirl3: *
4: Pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1135	61.0	358	2 T13017	hypothetical prote
2	1134	60.9	350	2 T05589	hypothetical prote
3	383	20.6	198	2 T20305	hypothetical prote
4	364.5	19.6	395	2 S66940	SGT1 protein - yea
5	341	18.3	444	2 T40307	hypothetical prote
6	327	17.6	469	2 T48783	related to SGT1 pr
7	223	12.0	533	2 E84858	phosphoprotein pho
8	193.5	10.4	572	2 H86257	protein F5011.2 [i
9	192	10.3	498	1 S52570	phosphoprotein pho
10	187	10.0	358	2 T00954	hypothetical prote
11	186	10.0	499	1 A55346	phosphoprotein pho
12	181.5	9.8	543	2 A38093	transformation-sen
13	180.5	9.7	473	1 T40391	phosphoprotein pho
14	177.5	9.5	589	2 A32567	stress-induced pro
15	176	9.5	569	2 S56558	stress-induced pro
16	174	9.3	349	2 T08782	hypothetical prote
17	174	9.3	526	1 T45058	phosphoprotein pho
18	169.5	9.1	513	1 S52571	phosphoprotein pho
19	163.5	8.8	346	2 S61991	hypothetical prote
20	163.5	8.8	591	2 T41531	activator of Hsp70
21	161.5	8.7	558	2 T48150	stress-induced pro
22	160	8.6	627	2 T04562	hypothetical prote
23	159.5	8.6	479	1 T46576	phosphoprotein pho
24	159.5	8.6	591	2 T51996	hypothetical prote
25	157.5	8.5	901	2 JC7111	tetratricopeptide
26	151	8.1	677	2 T45682	hypothetical prote
27	148.5	8.0	358	2 T37805	hypothetical prote
28	147	7.9	317	2 T37851	hypothetical prote
29	146.5	7.9	385	2 S40899	hypothetical prote

30	145.5	7.8	422	2 T24865	hypothetical prote
31	141.5	7.6	1979	2 JMW059	mtprd protein - mo
32	139	7.5	605	2 AF1917	hypothetical prote
33	139	7.5	781	2 F86457	unknown protein, 3
34	137.5	7.4	547	2 AE1884	hypothetical prote
35	136.5	7.3	222	2 F86424	unknown protein, 6
36	136	7.3	225	2 AB2539	hypothetical prote
37	132.5	7.1	320	2 T03899	hypothetical prote
38	130.5	7.0	297	2 T34141	hypothetical prote
39	130.5	7.0	1621	2 AB2255	72K mitochondrial
40	130	7.0	619	2 A36682	tetratricopeptide
41	130	7.0	2025	2 JC5020	extracellular matr
42	130	7.0	2055	2 T31110	hypothetical prote
43	129.5	7.0	427	2 T00960	class I heat-shock
44	129.5	7.0	542	2 AD1333	unc-45 protein - C
45	127.5	6.9	961	2 T32493	

ALIGNMENTS

RESULT 1

T13017

hypothetical protein F8L21.50 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T13017

submitted to the Protein Sequence Database, July 1999

A:Reference number: Z17587

A:Accession: T13017

A:Molecule type: DNA

A:Residues: 1-358 <BEV>

A:Cross-references: UNIPROT:Q9SUT5; EMBL:AL096882; GSPDB:GNO0062; ATSP:F8L21.50

A:Experimental source: cultivar Columbia; BAC clone F8L21

C:Genetics:

A:Gene: ATSP:F8L21.50

A:Map position: 4

A:Introns: 54/1, 77/2, 119/1, 161/2, 193/3, 215/3, 262/1, 288/3, 323/3

Query Match 61.0%; Score 1135; DB 2; Length 358;

Best Local Similarity 61.0%; Pred. No. 1.5e-69;

Matches 224; Conservative 49; Mismatches 76; Indels 18; Gaps 4;

QY	3	ASDLESKAKEAFVDDDFELATLYSQADAGPATADLVADRAQAHIKLGNYTEAVDANK	62
DB	2	AKELAEKAEAFLDVAVDLYSKAIDLDPNCAAFADRAQAQNIKIDNFTFVAVDANK	61
QY	63	ATELDPMHKAAYRKGACIKLEEYQTAKAALGLSSVAGSDRSFARLLKCDERIAEES	122
DB	62	AIELEPTLAKVLRGTACMKLEEYSTAKALEKASVAPNEPKFKMIDCDLRIAESE	121
QY	123	SQ-----APVKNVBEATVAATIEDKEDFTNMENTPPVIEP--PSKPKYRHNYNSATEVV	174
DB	122	KDLVQPMPSLPSSSTTTPLATEAD-----APPVTPAAPAKPMFHFYQKPEEAV	172
QY	175	LTFPAKVPADSVVDVDFEQMLSVIEVPGEPYHFORLPSKIIPECKYCVLSTKVEI	234
DB	173	VTFPAKVPKNVTYVFEQQLSVVDVAGEAYHLQRLFKIIPKCRFRVLTSTKVEI	232
QY	235	RLAKAEQVTTWTLDYSGRPKTPVKQISTPAETAPRPSYSSKAKDKDMLAEVKEEKE	294
DB	233	RLAKAEITWASLEY-GKQSVLPKPNVSSALSQRPVFPSSKPAKDWKLEAEVKKQKD	291
QY	295	EKLGDGAALNKFPRDIYKDADEDMERRAMKSVESNGTVLSTNWKDVGAKKVEGSPDGM	354
DB	292	EKLGDGAAMKFFSDIYSSADEDMERRAMKSPAESNGTVLSTNWKVEGTVKKVESTPPDGM	351
QY	355	ELKKWEY 361	
DB	352	ELKKWEY 358	

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QY	444	ATCTAGCCAGGCA	CCAGTAAGAATGTTGAGGCTACTGTGGCTGCTACTATTGAGGACAA	503
Db	445	ATCTAGCCAGGCA	CCAGTAAGAATGTTGAGGCTACTGTGGCTGCTACTATTGAGGACAA	504
QY	504	GGAGGATTTTCA	CAAAATATGGAGAAATACACCAACAGTGATAGAACCCCAAGCAACCAAA	563
Db	505	GGAGGATTTTCA	CAAAATATGGAGAAATACACCAACAGTGATAGAACCCCAAGCAACCAAA	564
QY	564	ATACAGGCATGA	CTACTACAACAGTGCCACAGAAAGTGCTACTGACAAATATTTGCTTAAGGG	623
Db	565	ATACAGGCATGA	CTACTACAACAGTGCCACAGAAAGTGCTACTGACAAATATTTGCTTAAGGG	624
QY	624	TGTTCTGCTGTA	TAGTGTAAGTCAATGATTTTGGTGAAACAGATGTTGAGTGATATCAATTGA	683
Db	625	TGTTCTGCTGTA	TAGTGTAAGTCAATGATTTTGGTGAAACAGATGTTGAGTGATATCAATTGA	684
QY	684	AGTTCTGCTGTA	GGAAGCAACCATACATTTTCAGGCCCGCTGTTTCTTAGATTTATCCCTGA	743
Db	685	AGTTCTGCTGTA	GGAAGCAACCATACATTTTCAGGCCCGCTGTTTCTTAGATTTATCCCTGA	744
QY	744	GAAATGCAAAAT	ATCAAGTCTTATCCAACAGGTTGAAATACGCTTGCAAAAGCTGAGCA	803
Db	745	GAAATGCAAAAT	ATCAAGTCTTATCCAACAGGTTGAAATACGCTTGCAAAAGCTGAGCA	804
QY	804	GGTGACATGGCA	CAACCCCTGGATATAGTGGGAAGACCAAGACTGTTCCTCCAGAGATTAAG	863
Db	805	GGTGACATGGCA	CAACCCCTGGATATAGTGGGAAGACCAAGACTGTTCCTCCAGAGATTAAG	864
QY	864	CACGCCAGCTGA	AAACAGGCCCAAGACCTTTCATACCCATCTTCAAAGGGCGAAAAGACTG	923
Db	865	CACGCCAGCTGA	AAACAGGCCCAAGACCTTTCATACCCATCTTCAAAGGGCGAAAAGACTG	924
QY	924	GGATAAATCTGA	AGCTGAAGTCAAAAAGGAGGAAGGAAGAAAACCTTGATGGTGATGC	983
Db	925	GGATAAATCTGA	AGCTGAAGTCAAAAAGGAGGAAGGAAGAAAACCTTGATGGTGATGC	984
QY	984	TGCATTGAAACA	AAATCTTTCCGTGACATCTACAAGGATGCTGATGAAGATATCGCGAGGCG	1043
Db	985	TGCATTGAAACA	AAATCTTTCCGTGACATCTACAAGGATGCTGATGAAGATATCGCGAGGCG	1044
QY	1044	CATGATGAAGT	CATTTCGTGGAATCAAAATGGCACTGTTCTCTCAACCAATTGGAAGAATGT	1103
Db	1045	CATGATGAAGT	CATTTCGTGGAATCAAAATGGCACTGTTCTCTCAACCAATTGGAAGAATGT	1104
QY	1104	TGGAGCAAGAAG	TAGTAGGAGGCCCCCTGATGGTATGAGCTCAAGAAAGTGGGAATA	1163
Db	1105	TGGAGCAAGAAG	TAGTAGGAGGCCCCCTGATGGTATGAGCTCAAGAAAGTGGGAATA	1164
QY	1164	CTAAAGTTTGGAC	TGCCGCTCTTTTGTAAATCTGAGGCTTGGAAACTATGACCTAAATCT	1223
Db	1165	CTAAAGTTTGGAC	TGCCGCTCTTTTGTAAATCTGAGGCTTGGAAACTATGACCTAAATCT	1224
QY	1224	GCCCAACCATAG	TGCGCATGAGCTTGCTTGGTAAAGTCTCTGCTTTTGTAAAGCTTTCTGTA	1283
Db	1225	GTCACCCATAGT	AGCTGAGCTTGGTAAAGTCTCTGCTTTTGTAAAGCTTTCTGTA	1284
QY	1284	TGACAGTCTAGC	GTGCTGAGTGCTACTTGGCGTAGCTTTTGATGGACATAGGTATGC	1343
Db	1285	TGACAGTCTAGC	GTGCTGAGTGCTACTTGGCGTAGCTTTTGATGGACATAGGTATGC	1344
QY	1344	TATTATGTGGTAT	CGACCCCGAACCATCTGTGGTATCAAAGACAGCAAACTATAATGCTAT	1403
Db	1345	TATTATGTGGTAT	CGACCCCGAACCATCTGTGGTATCAAAGACAGCAAACTATAATGCTAT	1404
QY	1404	GGAATGCCATT	CTTTTGGTCTAAAA	1430
Db	1405	GGAATGCCATT	CTTTTGGTCTAAAG	1431

RESULT 3

US-10-425-114-25244
; Sequence 25244, Application US/10425114

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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acids and Methods of Invention
FILE OF INVENTION: Plants and Methods of Invention
CURRENT APPLICATION NUMBER: US 2003-04-12
CURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 25244
LENGTH: 1450
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: I
US-10-425-114-25244

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Query Match	95.8%	Score 1394.2	DB 17	Length 1450
Best Local Similarity	99.4%	Pred. No. 0		
Matches 1399	Conservative 0	Mismatches 8	Indels 0	Gaps 0
QY 24	AGTCATCGTCTGGTCTGCGCCGCGAGGGCGCAGACGCCCAAGCCCGAAGGGCGGCCAT	83		
Db 31	AGTCATCGTCTGGTCTGCGCCGCGAGGGCGCAGACGCCCAAAACCGGAAGGGCGGCCAT	90		
QY 84	GGCCGCGTCCGATCTCGAGAGCAAGGCCAAGGAGGGCCTTCGTCCAGCACGACTTCGAGCT	143		
Db 91	GGCCGCGTCCGATCTCGAGAGCAAGGCCAAGGAGGGCCTTCGTCCAGCACGACTTCGAGCT	150		
QY 144	GGCCACCGAGCTCTACAGCCAGGCGCATCGACGGCGGGCCGCCACCGCCGACTCTTATGC	203		
Db 151	GGCCACCGAGCTCTACAGCCAGGCGCATCGACGGCGGGCCGCCACCGCCGACTCTTATGC	210		
QY 204	CGACCGCGCCCGAGCGGCACATCAAGCTTCGGCAACTACACTAGAGGCTGTGCGGAGTGTAA	263		
Db 211	CGACCGCGCCCGAGCGGCACATCAAGCTTCGGCAACTACACTAGAGGCTGTGCGGAGTGTAA	270		
QY 264	CAAAAGCAATTGAGCTTGATCTTATGATGCATAAAGCTTACTACCGAAAAGGTGCTGCATG	323		
Db 271	CAAAAGCAATTGAGCTTGATCTTATGATGCATAAAGCTTACTACCGAAAAGGTGCTGCATG	330		
QY 324	CATTAGAGCTTGAGAAATACCAACTCGAAAGGCTGCTCTTGGTTCGGTCTCTTATGC	383		
Db 331	CATTAGAGCTTGAGAAATACCAACTCGAAAGGCTGCTCTTGGTTCGGTCTCTTATGC	390		

Qy	384	ATCAGGCGATTCAAGGTTTGGCTCGTCTATTGAAGGAATGTGATGAGCGCATCGCTGAGGA	443
Db	391	ATCAGGCGATTCAAGGTTTGGCTCGTCTATTGAAGGAATGTGATGAGCGCATCGCTGAGGA	450
Qy	444	ATTAGCCAGGCAACCGATTAAAGAAATGTTGAGGCTACTGTGGCTGCTACTATTGAGGACAA	503
Db	451	ATTAGCCAGGCAACCGATTAAAGAAATGTTGAGGCTACTGTGGCTGCTACTATTGAGGACAA	510
Qy	504	GGAGGATTTACAAAATATGGAGNATACACCAACAGTGATAGAAACCCCAAGCAAAACCAAA	563
Db	511	GGAGGATTTACAAAATATGGAGNATACACCAACAGTGATAGAAACCCCAAGCAAAACCAAA	570
Qy	564	ATACAGGCATGACTACTACAAACAGTGCACAGAAAGTGGTACTGACAAATATTTGCTAAGGG	623
Db	571	ATACAGGCATGACTACTACAAACAGTGCACAGAAAGTGGTACTGACAAATATTTGCTAAGGG	630
Qy	624	TGTTCTGCTGATAGTGTAGTCAATGATTTTGGTGAAACAGATGTTGAGTGTATCCATTGA	683
Db	631	TGTTCTGCTGATAGTGTAGTCAATGATTTTGGTGAAACAGATGTTGAGTGTATCCATTGA	690
Qy	684	AGTTCTGTGTGAAGAACCATACATTTTCAGCCCCGTCTGTTTTCTAAGATATATCCCTGA	743
Db	691	AGTTCTGTGTGAAGAACCATACATTTTCAGCCCCGTCTGTTTTCTAAGATATATCCCTGA	750

Db	1053	GTGGAGACCAAGACTGTTCCCGAAGATAGACCGCAGCTGAAACAGCCCCCAAGAC	1112
Qy	890	CTTCATACCACTCTTCAAGCGCAAAAAGA CTGGATAAATCGGAAGCTGAAAGTCAAAA	949
Db	1113	CTTCATACCACTCTTCAAGCGCAAAAAGA CTGGATAAATCGGAAGCTGAAAGTCAAAA	1172
Qy	950	AGGAGGAGAAGGAAGAAACCTTGATGCTGATCTGCATTTGAACAAATCTTCCGTCACA	1009
Db	1173	AGNGGAGAGGAAGAAACCTTGATGCTGATCTGCATTTGAACAAATCTTCCGTCACA	1232
Qy	1010	TCTACAAGGATGCTGATGAAGATATGCGGAGGCCATGATGAAGTCAATTCGTGGAATCAA	1069
Db	1233	TCTACAAGGATGCTGATGAAGATATGCGGAGGCCATGATGAAGTCAATTCGTGGAATCAA	1292
Qy	1070	ATGCACTGTTCTCTCAACCAATTTGNAAGATGTTGGAGCAAAAGAGGTAGAGGGAGCC	1129
Db	1293	ATGCACTGTTCTCTCAACCAATTTGNAAGATGTTGGAGCAAAAGAGGTAGAGGGAGCC	1352
Qy	1130	CCGCTGATGTTGAGAGCTCAAGAAGTGGGAATACTAAAGTTTGGAGCTGCCCGCTCTTTTG	1189
Db	1353	CCGCTGATGTTGAGAGCTCAAGAAGTGGGAATACTAAAGTTTGGAGCTGCCCGCTCTTTTG	1412
Qy	1190	TAAATCCAGTCTTGGNAACTATGACCTAAATCTTGCCCAACCAATAGTGCATGAGCTTGC	1249
Db	1413	TAAATCCAGTCTTGGNAACTATGACCTAAATCTTGCCCAACCAATAGTGCATGAGCTTGC	1472
Qy	1250	TTGGTTAAGTCTCTGCTTTTGAAGCTTTCTGTATGACAGCTCTAGCGGTGTCTGAGTGC	1309
Db	1473	TTGGTTAAGTCTCTGCTTTTGAAGCTTTCTGTATGACAGCTCTAGCGGTGTCTGAGTGC	1532
Qy	1310	TACTTGCCTGAGCTTTTGATGGACATAGGATGCTATTATGTGGTATCGACCCCGCAACCA	1369
Db	1533	TACTTGCCTGAGCTTTTGATGGACATAGGATGCTATTATGTGGTATCGACCCCGCAACCA	1592
Qy	1370	TCGTGCTATCAAGACAGCAAACTAATGATGGAATGCCTATTCTTTTGGTCTAAA	1429
Db	1593	TCGTGCTATCAAGACAGCAAACTAATGATGGAATGCCTATTCTTTTGGTCTAAA	1652
Qy	1430	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	1455
Db	1653	AAAAAAAAAAAAAAAAAGCGCCAAAAA	1678

RESULT 5

```

US-10-425-114-24871
; Sequence 24871, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 24871
; LENGTH: 1649
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-210-C7_FLI
US-10-425-114-24871

```

```
Query Match      81.0%; Score 1179; DB 17; Length 1649;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 1403; Conservative 0; Mismatches 0; Indels 214; Gaps 1;
```

Qy	24	AGTCATCGTCTGTCGTCGCCGCGAGCGCGGAGACGCCCAAGCGCGGAGCGGGCGCCAT	83
Db	33	AGTCATCGTCTGTCGTCGCCGCGAGAGCGCGACGCGCCAAAGCGCGAAGGGCGCCAT	92
Qy	84	GCCGCGTCGGATCTCGGAGACAAAGGCCAAAGAGCCCTTCGTCGACGACGACTTCGAGCT	143
Db	93	GCCGCGTCGGATCTCGGAGACAAAGGCCAAAGAGCCCTTCGTCGACGACGACTTCGAGCT	152
Qy	144	GGCCACCGAGCTCTACAGCCAGGCGCATCGACCGCGGCCGCCCAACCGCGACCTCTATGC	203
Db	153	GGCCACCGAGCTCTACAGCCAGGCGCATCGACCGCGGCCGCCCAACCGCGACCTCTATGC	212
Qy	204	CGACCGGCCCGAGCGGCACATCAAGCTCGGCAACTACAGAGCTGTGGCGATGCTAA	263
Db	213	CGACCGGCCCGAGCGGCACATCAAGCTCGGCAACTACAGAGCTGTGGCGATGCTAA	272
Qy	264	CAAGCAATGAGCTTCGATCTATGATGCATAAAGCTTACTACCGGAAGTGTGCGCATG	323
Db	273	CAAGCAATGAGCTTCGATCTATGATGCATAAAGCTTACTACCGGAAGTGTGCGCATG	332
Qy	324	CATTAAAGCTTGAAGAAACCAAACTGCAAAAGCGCTGCTCTTGAGTTGGTTCCTTATATGC	383
Db	333	CATTAAAGCTTGAAGAAACCAAACTGCAAAAGCGCTGCTCTTGAGTTGGTTCCTTATATGC	392
Qy	384	ATCAGGCGATTCAGAGTTTGGTCTGCTATTTGAAGGAATGTGATGAGCGCATCGCT----	438
Db	393	ATCAGGCGATTCAGAGTTTGGTCTGCTATTTGAAGGAATGTGATGAGCGCATCGCTGTGTA	452
Qy	439	-----	438
Db	453	GAATAATTAATTCAGCAGTGTGTGTATCTGCTGTGTGTGTGTGGGTCTTGGGTATGC	512
Qy	439	-----	438
Db	513	AATGTGTGTCATGCTATTTTCTGACGATATGAGTCCACTTAGCTGCCTTCTCTGAGAAT	572
Qy	439	-----	438
Db	573	GTTTGTAGCAGCCTTGTAGACTGGGGATGATTATGTTTTCAGCTTAATCATCTCATACTA	632
Qy	439	-----GAGGAATCTAGCCAGGCCACCGTAAGATG	469
Db	633	CTGTCTCATGTTATTTTGTGTTATGTTTCCAGAGGAATCTAGCCAGGCCACCGTAAGATG	692
Qy	470	TTGAGGCTACTGTGGCTGTCTACTATTGAGCACAAGGAGGATTTCCAAAATATGGAGAATA	529
Db	693	TTGAGGCTACTGTGGCTGTCTACTATTGAGCACAAGGAGGATTTCCAAAATATGGAGAATA	752
Qy	530	CACCAACAGTGATAGAAACCCCAAGCAAAACCAAAATACAGGCACTACTACTACACAGTG	589
Db	753	CACCAACAGTGATAGAAACCCCAAGCAAAACCAAAATACAGGCACTACTACTACACAGTG	812
Qy	590	CCACAGAGTGATCTGACAAATATTTGCTAAGGGTGTTCCTGCTGATAGTGTAGTCAATTG	649
Db	813	CCACAGAGTGATCTGACAAATATTTGCTAAGGGTGTTCCTGCTGATAGTGTAGTCAATTG	872
Qy	650	ATTTTGTGTGAACAGATGTTGAGTGATCCATTTGAAGTTTCTTGTGTGAAGAACCATACCAT	709
Db	873	ATTTTGTGTGAACAGATGTTGAGTGATCCATTTGAAGTTTCTTGTGTGAAGAACCATACCAT	932
Qy	710	TTCAGCCCCGTCTGTTTTCTTAAGATTATCCCTGAGAAATGCAAAATATCAAGCTTTATCCA	769
Db	933	TTCAGCCCCGTCTGTTTTCTTAAGATTATCCCTGAGAAATGCAAAATATCAAGCTTTATCCA	992
Qy	770	CCAAGGTTGAATACCGCTTGAAAAGCTGAGCAGGTGACATGGACAACCTGTGATTTATA	829
Db	993	CCAAGGTTGAATACCGCTTGAAAAGCTGAGCAGGTGACATGGACAACCTGTGATTTATA	1052
Qy	830	GTGGAAGACCAAGACTGTTTCCCGACAAGATAGCAGCCAGCTGAAACAGCCCCAGAC	889
Db	1053	GTGGAAGACCAAGACTGTTTCCCGACAAGATAGCAGCCAGCTGAAACAGCCCCAGAC	1112
Qy	890	CTTTCATACCCTCTTTCAAAAGGGCGAAAAGACTGGGATTAACCTGGAGTGTGAAGTCAAAA	949

1300 GTCTGAGTGCTACTTCGCGTAGCTTTTGATGGACATA-----GATAGCTATTATGTGCTA 1355
1321 GTCTGAGTGTGCTTCGCGTAGTTTTCGATGGACATATCATGGTAGCTATCTCTGTGCTA 1380
1356 TCGACCCCGAACCATCTGTGTGTATCAAAGACAG-CAAACTATAATGTATGGAATGCGCTAT 1414
1381 TC-----AACATCTGTGTGTAACAAAGACAGATAACTATATCTGTGGAATGCGCTAT 1432
1415 TCTTTTGGTCTAAAA 1431
1433 TCTTTTGGTCTAAGA 1449

RESULT 7

```

US-10-425-114-25845
/ Sequence 25845, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 25845
/ LENGTH: 1361
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3960-013-B4_FLI
US-10-425-114-25845

```

Query Match	72.0%	Score 1047	DB 17	Length 1361
Best Local Similarity	92.3%	Pred. No. 2.1e-285		
Matches 1125	Conservative 0	Mismatches 90	Indels 4	Gaps 2
QY	54	GCAGAGCCGCCAAGCCGAAGGGCGGCCATGTGGCGCGTTCGGAATCTGAGAGCAAGGCCAA	113	
Db	71	GCAGAGCCCGAGAGCCGAGGAGCGCATGTGGCGCGTTCGGAATCTGAGAGCAAGGCCAA	130	
QY	114	GGAGGCGCTTCGTTCGAGCGAGCACTTCGAGCTGGGCCACCGAGCTCTACAGCCAGGCCATCGA	173	
Db	131	GGAGGCGCTTCGTTCGAGCGAGCACTTCGAGCTGGGCCCGGAATCTCTACAGCGAGGCCATCGA	190	
QY	174	CGCGGGCGCGCCACCGGCCGACCTCTATGCGCGACCGCGCCAGCGCCACATCAAGCTCGG	233	
Db	191	CGCGGGCGCGCCACCTGCCGATCTTACGCGGACCGCGCCAGCGCCACATCAAGCTCGG	250	
QY	234	CAACTACATGAGGCTGTGGCGGATGCTAACAAAGCAATTGAGCTTTGATCTCTATGATGCA	293	
Db	251	CAACTACATGAGGCTGTGGCAGATGCTAACAAAGCAATTGGTCTTGATCTCTACATGCA	310	
QY	294	TAAAGCTTACTACCGGAAAGGTGCTCGATGCATTAAAGCTTGAAGATACAAACTGCCAA	353	
Db	311	TAAAGCTTACTACCGGAAAGGTGCTCGATGCATTAAAGCTTGAAGATATACAAACTGCCAA	370	
QY	354	GGCTGCTCTTGAGTTGGGTTCTTTATGCATCAGCGGATTCAGAGTTTGCTCGCTATT	413	
Db	371	GGCTGCTCTTGAGTTAGGTTCTTCTATGCACGAGCGATTCAAGTTTACCCTGCTATT	430	
QY	414	GAGGAACTGTATGAGCGCATCGCTGAGGAATCTAGCCAGGACCCAGTAAGAAGTTTGA	473	
Db	431	GAGGAACTGTATGAGTGCATTGCTGAGGAATCTAGCCAGGACCCAGCAAGAAGTGTGA	490	
QY	474	GCGTACTGTGGCTGCTACTATTGAGGACAAGGAGGATTTCACAAATATGGAGAATACACC	533	
Db	491	GCGTCTGTAGTGTCTACTGTTGAGACAAGGAGGATTCGCAAAATATGGGATAATACACC	550	

RESULT 8

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US-10-425-14-22598
; Sequence 22598, Application US/10425114
; Publication NO. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabasta, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22598
; LENGTH: 1490

```

/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3591-005-B5_FLI
US-10-425-114-22598

Query Match 72.0%; Score 1047; DB 17; Length 1490;
Best Local Similarity 92.3%; Pred. No. 2.2e-285;
Matches 1125; Conservative 0; Mismatches 90; Indels 4; Gaps 2;

QY	54	GCAGAGCCCAAGCGGAGGCGCGCATGGCGCGTGGATCTGGAGAGCAAGGCCAA	113
DB	139	GCAGAGCCCAAGCGGAGGCGCGCATGGCGCGTGGATCTGGAGAGCAAGGCCAA	198
QY	114	GGAGGCGCTTGGTGGAGCAGCACTTCGAGCTGGCCACCGAGCTCTACAGCCAGCCATCGA	173
DB	199	GGAGGCGCTTGGTGGAGCAGCACTTCGAGCTGGCCACCGAGCTCTACAGCCAGCCATCGA	258
QY	174	CGCGGCGCCGCGCACCGCGCACTCTATGCGGACCGCGCCAGCGGCACATCAAGCTCGG	233
DB	259	CGCGGCGCCGCGCACCGCGCACTCTATGCGGACCGCGCCAGCGGCACATCAAGCTCGG	318
QY	234	CRACTACACTGAGCTGTGGCGGATCTAACAGCAATTCGATCTCTATGATGCA	293
DB	319	CAACTACACTGAGCTGTGGCGGATCTAACAGCAATTCGATCTCTATGATGCA	378
QY	294	TAAAGCTTACTACCGGAAAGGTGCTGCATGCATTAAGCTTTGAAGAAATACCAAACTGC	353
DB	379	TAAAGCTTACTACCGGAAAGGTGCTGCATGCATTAAGCTTTGAAGAAATACCAAACTGC	438
QY	354	GGCTGCTCTTGGTGGTCTTCTTATGATCATGAGCGATTCAGGTTGCTCGTCTATT	413
DB	439	GGCTGCTCTTGGTGGTCTTCTTATGATCATGAGCGATTCAGGTTGCTCGTCTATT	498
QY	414	GAAGGATGTGAGCGCATCTGAGGATCTAGCCAGGCGCCAGTAAGATGTGA	473
DB	499	GAAGGATGTGAGCGCATCTGAGGATCTAGCCAGGCGCCAGTAAGATGTGA	558
QY	474	GGCTACTGTGGCTGCTACTATTGAGGACAAAGGAGGATTCACAAATATGAGAAATACACC	533
DB	559	GGCTACTGTAGCTGCTACTATTGAGGACAAAGGAGGATTCACAAATATGAGAAATACACC	618
QY	534	ACGATGATAGAACCCCAAGCAACCAAAATACAGCGCATGACTATCAACAGTGGCCAC	593
DB	619	GCCAGTGGTAGAACCCCAAGCAACCAAAATATAGGCATGACTACTACAACTGGCCAC	678
QY	594	AGAGTGGTACTGACATATTGCTAAGGTTCTCTGCTGATAGTGTAGTCTATTGATT	653
DB	679	AGAGTGGTCTCAATATATGCTAAGGTTCTCTGCTGATAGTGTAGTCTATTGATT	738
QY	654	TGGTGAACAGATGTTGATGTATCCATTGAAGTTCTGTTGAAGAACCATACCAATTTCA	713
DB	739	TGGTGAACAGATGTTGATGTATCCATTGAAGTTCTGTTGAAGAACCATACCAATTTCA	798
QY	714	GCCCGCTGTGTTTCTAAGATATTCCTGAGAAATGCAATATCAAGTCTTATCCACCA	773
DB	799	GCCCGCTGTGTTTCTAAGATATTCCTGAGAAATGCAAGTATCAAGTCTTATCCACCA	858
QY	774	GTTTGAATACGCTTCCAAAGCTGAGCGTGCATGACACACCTCGGATATATAGTG	833
DB	859	GTTTGAATACGCTTCCAAAGCTGAGCGTGCATGACACACCTCGGATATATAGTG	918
QY	834	AAGACCAAGAGCTGTCCCAAGAGATAAGCACCCAGCTGAAACAGCCCAAGACCTTC	893
DB	919	AAGACCAAGAGCTGTCCCAAGAGATAAGCACCCAGCTGAAACAGCCCAAGACCTTC	978
QY	894	ATACCCATCTTCAAAGCGGAAAAAGACTGGGATAAATCTGGAAGCTGAAGTCAAAAGGA	953
DB	979	ATACCCATCTTCAAAGCTCAAAAGGAGCTGGGATAAATCTGGAAGCTGAAGTCAAAAGGA	1038
QY	954	GGAGAGGAGAAAACTTGTGATGTGCTGCAATGCAAAATCTTCCGTGACATCTA	1013
DB	1039	GGAGAGGAGAAAACTTGTGATGTGCTGCAATGCAAAATCTTCCGTGATATCTA	1098

QY	1014	CAAGATGCTGATGAAGATATGCGAGGGCCATGATGATGATCATTCGTGGAATCAATGG	1073
DB	1099	CAAGATGCTGATGAAGATATGCGAGGGCCATGATGATGATCATTCGTGGAATCAATGG	1158
QY	1074	CACTGTTCTCTCAACCAATTGGAAAGATGTTGGAGCAAGAGGTAGAGGAGGAGCCCCC	1133
DB	1159	TAACGTTCTCTCAACCAATTGGAAAGATGTTGGATCAAGAGCGGTGGAAGCGAGCCCTCC	1218
QY	1134	TGATGGTATGAGCTCAAGAGTGGGAATATCAAAAGTTTGGACTGCCCCCTCTTTGTAAA	1193
DB	1219	TGATGGTATGAGCTCAAGAGTGGGAATATCAAAAGTTTGGACTGCCCCCTCTTTGTAAA	1276
QY	1194	TCAGGCTTGTGAAACTATGACCTAATTCGCCCCACCA--TAGTGCCATGAGCTTGT	1251
DB	1277	TCAGGCTTGTGAACTATGACCTAATTCGCCCCACCA--TAGTGCCATGAGCTTGT	1336
QY	1252	GGTTAAGTCTCTGCTTTTG	1270
DB	1337	AAGTGTGTGTGTTTTTG	1355

RESULT 9

US-10-425-115-18041
; Sequence 18041, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222) B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 18041
; LENGTH: 1519
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116456C.1
US-10-425-115-18041

Query Match 71.9%; Score 1046; DB 18; Length 1519;
Best Local Similarity 92.3%; Pred. No. 4.3e-285;
Matches 1124; Conservative 0; Mismatches 90; Indels 4; Gaps 2;

QY	54	GCAGAGCCCAAGCGGAGGCGCCATGGCGCGTCCGATCTGGAGAGCAAGGCCAA	113
DB	139	GCAGAGCCCAAGCGGAGGCGCCATGGCGCGTCCGATCTGGAGAGCAAGGCCAA	198
QY	114	GGAGGCTTTCGTGCGAGCAGCTTCGAGCTGGCCACCGAGCTCTACAGCAGGCCATCGA	173
DB	199	GGAGGCTTTCGTGCGAGCAGCTTCGAGCTGGCCACCGAGCTCTACAGCAGGCCATCGA	258
QY	174	CGCGGCGCCGCGCACCGCGCACTCTATGCGGACCGCGCCAGCGGCACATCAAGCTCGG	233
DB	259	CGCGGCGCCGCGCACCGCGCACTCTATGCGGACCGCGCCAGCGGCACATCAAGCTCGG	318
QY	234	CAACTACACTGAGCTGTGGCGGATCTAACAGCAATTCGATCTGATGATGCA	293
DB	319	CAACTACACTGAGCTGTGGCGGATCTAACAGCAATTCGATCTGATGATGCA	378
QY	294	TAAAGCTTACTACCGGAAAGGTGCTGCATGCAATTAAGCTTGAAGAAATACCAAACTGCAA	353
DB	379	TAAAGCTTACTACCGGAAAGGTGCTGCATGCAATTAAGCTTGAAGAAATACCAAACTGCAA	438
QY	354	GGCTGCTCTTGGATGGGTTCTTCTTATGATCAGCGGATTCAGGTTTGTGCTGCTATT	413
DB	439	GGCTGCTCTTGGATGGGTTCTTCTTATGATCAGCGGATTCAGGTTTGTGCTGCTATT	498

414 GAAGGAATGTGATGAGCGCATCGCTGAGGAATCTTAGCCAGGACCAAGTAAGAATGTTGA 473
499 GAAGGAATGTGATGAGCGCATCGCTGAGGAATCTTAGCCAGGACCAAGTAAGAATGTTGA 558
474 GCTACTGTGGCTGCTACTATTGAGGACCAAGGAGATTTCACAAATATGGAGATACAC 533
559 GCTCTCTGTAGCTGCTACTATTGAGGACCAAGGAGATTTCGCAATATGGATATACAC 618
534 ACCAGTGATAGAACCCCAAGCAACCAACCAATATACAGGATGACTACTCAACAGTGCCAC 593
619 GCCAGTGATAGAACCCCAAGCAACCAACCAATATATAGGATGACTACTCAACAGTGCCAC 678
594 AGAAGTGATGATGAGCGCATCGCTGAGGAATCTTAGCCAGGACCAAGTAAGAATGTTGA 713
679 AGAAGTGATGATGAGCGCATCGCTGAGGAATCTTAGCCAGGACCAAGTAAGAATGTTGA 798
654 TGGTGAACAGATGTTGAGTATGATGAGGAATCTTAGCCAGGACCAAGTAAGAATGTTGA 773
739 TGGTGAACAGATGTTGAGTATGATGAGGAATCTTAGCCAGGACCAAGTAAGAATGTTGA 798
714 GCCCGCTGCTGTTTCTAAGATTATCCCTGAGAAATGCAATATCAAGTCTTTATCCACAA 773
799 GCCCGCTGCTGTTTCTAAGATTATCCCTGAGAAATGCAATATCAAGTCTTTATCCACAA 858
774 GGTGAAATAGCGCTTCCCAAGAGTGAAGGATGAGGATGAGGATGAGGATGAGGATGAGG 833
859 GGTGAAATAGCGCTTCCCAAGAGTGAAGGATGAGGATGAGGATGAGGATGAGGATGAGG 918
834 AGACCAAGATGTTTCCCAAGAGTGAAGGATGAGGATGAGGATGAGGATGAGGATGAGG 953
919 AGACCAAGATGTTTCCCAAGAGTGAAGGATGAGGATGAGGATGAGGATGAGGATGAGG 978
894 ATACCAATCTTCAAGAGTGAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 953
979 ATACCAATCTTCAAGAGTGAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1038
954 GGAAGAGGAG 1013
1039 GGAAGAGGAG 1098
1014 CAAGGATGCTGATGAGAGATGCGAGGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1073
1099 CAAGGATGCTGATGAGAGATGCGAGGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1158
1074 CACTGTTCTCTCAACCAATGGAAGATGTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1133
1159 TACCGTTCTCTCAACCAATGGAAGATGTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1218
1134 TGATGATGAGGATCAAGAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAG 1193
1219 TGATGATGAGGATCAAGAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAG 1276
1194 TCCAGGCTTGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1251
1277 TCCAGGCTTGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1336
1252 GGTAAAGTCTGCTGTTTT 1269
1337 AAGTGTGTGTGTTTTT 1354

RESULT 10
US-10-739-930-4858/c
Sequence 4858, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 4858
LENGTH: 2471
TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(2471)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: TRIAB-23APR03-CLUSTER396_1
US-10-739-930-4858

Query Match 51.8%; Score 753; DB 18; Length 2471;
Best Local Similarity 79.3%; Pred. No. 5.6e-202;
Matches 938; Conservative 0; Mismatches 200; Indels 45; Gaps 2;

QY 61 CCCAAGCCCGAAGGGCGCCATGCGCGCTCGAGTCTGGAGAGCAAGGCGCAGAGGCC 120
Db 2303 CTCGACGCGACATGCGCGCGCGCGCTCGAGTCTGGAGAGCAAGGCGCAGAGGCC 2244
QY 121 TTGCTCGAGCAGCAGCTTCGAGCTGGCCACCGAGCTCTACAGCAGGCGCATCGAGCGCG 180
Db 2243 TTGCTCGAGCAGCAGCTTCGAGCTGGCCACCGAGCTCTACAGCAGGCGCATCGAGCGCG 2184
QY 181 CCGCCACCGCGCACCTCTATGCCGACCGCGCGCGCGCACATCAAGCTCGGCACTAC 240
Db 2183 CCGCCACCGCGCACCTCTATGCCGACCGCGCGCGCGCACATCAAGCTCGGCACTAC 2124
QY 241 ACTGAGCTGTGGCGGATGCTTAAAGCAATTTGAGCTTGCCTATGATGCAATAAAGCT 300
Db 2123 ACTGAGCTGTGATGCTGATGCTTAAAGCAATTTGAGCTTGCCTATGATGCAATAAAGCT 2064
QY 301 TACTACCGAAGAGTGTGCTGATGCTTAAAGCAATTTGAGCTTGCCTATGATGCAATAAAGCT 360
Db 2063 TACTACCGAAGAGTGTGCTGATGCTTAAAGCAATTTGAGCTTGCCTATGATGCAATAAAGCT 2004
QY 361 CTGAGTGTGGTCTTCTTATGCTATGCTGAGGATCTAGCCAGGACCAAGTAAAGTAAAGGAA 420
Db 2003 CTGAGTGTGGTCTTCTTATGCTATGCTGAGGATCTAGCCAGGACCAAGTAAAGTAAAGGAA 1944
QY 421 TGTGATGAGCGATCGCTGAGGATCTAGCCAGGACCAAGTAAAGTAAAGTAAAGTAAAGGAA 480
Db 1943 TGTGATGATCGTATGCTGAGGAGCTAGCCAGGACCAAGTAAAGTAAAGTAAAGTAAAGGAA 1884
QY 481 GTGGCT-----GCTACTATTGAG 498
Db 1883 GTGGCTCAGCTACATCTTCGGGGGCACTCTTCGGGGGCACTCTTCGGGGGCACTCTTCGGGGGCACT 1824
QY 499 GACAGGAGGATTTCACAAAATATGAGAGATACACCCAGGATGATAGACCCCGCAGCAAA 558
Db 1823 GAGGACGAGGATGTCAAATATGAGAGATGTCAGCCAGGATGATAGACCCCGCAGCAAA 1764
QY 559 CCAAAATACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
Db 1763 CCAAAATACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1704
QY 619 AAGGCTGCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 678
Db 1703 AAGGCTGCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1644
QY 679 ATTGAAGTCTCTGCTGAGAGACCATACCATTTTCAGCCCGCTGCTGCTTTCTAAGATTATC 738
Db 1643 ATTGAAGTCTCTGCTGAGAGACCATACCATTTTCAGCCCGCTGCTGCTTTCTAAGATTATC 1584
QY 739 CTTGAGAAATGCAAAATATCAAGTCTTATCCCAAGGTTGAAATACGCTTTCGAAAGGCT 798
Db 1583 CCAGATAAGTCAAGTATATCTGTTGTTCTTCAAAAGGTTGAAATGCTTTCGAAAGGCT 1524
QY 799 GAGCAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 858
Db 1523 GAGCAGTAACTTGGACATCATTTGATTTATCTGTTAAACCAAG---GCTCTCAGAG 1467
QY 859 ATAAGCAGCGCAGCTGAAACAGCCCAAGACCTTTCATACCCATCTTCAAGGCGGAAAAA 918

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 23, 2005, 03:11:06 ; Search time 685.535 Seconds
(without alignments)
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Perfect score: 1086
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score-distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1084.4	99.9	1444	17	US-10-425-114-15440 Sequence 15440, A
2	1084.4	99.9	1450	17	US-10-425-114-25244 Sequence 25244, A
3	1084.4	99.9	1755	18	US-10-425-115-18040 Sequence 18040, A
4	988.2	91.9	1537	18	US-10-767-701-13951 Sequence 13951, A
5	977.6	90.0	1361	17	US-10-425-114-25845 Sequence 25845, A
6	977.6	90.0	1490	17	US-10-425-114-22598 Sequence 22598, A
7	977.6	90.0	1519	18	US-10-425-115-18041 Sequence 18041, A
8	862	79.4	1649	17	US-10-425-114-24871 Sequence 24871, A
9	862	79.4	1706	18	US-10-425-115-18039 Sequence 18039, A
10	736.6	67.8	2471	18	US-10-739-930-4858 Sequence 4858, A
11	698.2	64.3	1569	18	US-10-437-963-37229 Sequence 37229, A

12	490	45.1	571	16	US-10-074-473-2	Sequence 2, Appli
13	476.8	43.9	1691	17	US-10-424-599-65599	Sequence 65699, A
14	474.4	43.7	1598	17	US-10-424-599-81927	Sequence 81927, A
15	416.6	38.4	483	17	US-10-424-599-118531	Sequence 118531, A
16	332.8	30.6	1674	17	US-10-424-599-98272	Sequence 98272, A
17	286	26.3	287	9	US-09-294-093B-571	Sequence 571, App
18	243.4	22.4	1029	17	US-10-424-599-81933	Sequence 81933, A
19	221.8	20.4	585	18	US-10-021-323-2492	Sequence 2492, Ap
20	217.8	20.1	534	18	US-10-021-323-14417	Sequence 14417, A
21	216.4	19.9	272	9	US-09-294-093B-4704	Sequence 4704, Ap
22	201.6	18.6	851	17	US-10-424-599-75856	Sequence 75856, A
23	194.4	17.9	528	18	US-10-021-323-14351	Sequence 14351, A
24	183.6	16.9	573	18	US-10-021-323-2546	Sequence 2546, Ap
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26	180.6	16.6	656	17	US-10-424-599-98270	Sequence 98270, A
27	175.4	16.2	523	18	US-10-021-323-15961	Sequence 15961, A
28	156.4	14.4	1264	17	US-10-264-049-918	Sequence 918, App
29	156.4	14.4	1366	16	US-10-287-218-33	Sequence 33, Appl
30	156.4	14.4	1366	18	US-10-474-291-33	Sequence 33, Appl
31	156.4	14.4	1555	18	US-10-335-053-99	Sequence 99, Appl
32	156.4	14.4	1776	18	US-10-357-930-22330	Sequence 22330, A
33	156.4	14.4	1776	18	US-10-357-930-28174	Sequence 28174, A
34	156.4	14.4	2053	10	US-09-983-802-45	Sequence 45, Appl
35	156.4	14.4	2053	10	US-09-984-490-45	Sequence 45, Appl
36	156.4	14.4	2053	11	US-09-973-278-82	Sequence 82, Appl
37	148.6	13.7	291	9	US-09-294-093B-3135	Sequence 3135, Ap
38	141.4	13.0	409	9	US-09-770-423-621	Sequence 621, App
39	129.2	11.9	481	10	US-09-770-961-929	Sequence 929, App
40	125	11.5	388	16	US-10-074-473-3	Sequence 3, Appl1
41	106.8	9.8	479	17	US-10-424-599-25942	Sequence 25942, A
42	106	9.8	432	17	US-10-424-599-49836	Sequence 49836, A
43	94.4	8.7	317	17	US-10-424-599-41142	Sequence 41142, A
44	93.2	8.6	672	17	US-10-260-238-1154	Sequence 1154, Ap
45	93.2	8.6	672	18	US-10-437-963-43909	Sequence 43909, A

ALIGNMENTS

RESULT 1
US-10-425-114-15440
; Sequence 15440, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 15440
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3059-061-D10_FLI
US-10-425-114-15440

Query Match 99.9% Score 1084.4; DB 17; Length 1444;
Best Local Similarity 99.9%; Pred No. 5.3e-313;
Matches 1085; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGGCCGCGTCGGATCTGGAGACCAAGGCCAAGGAGCGCTTCGTCGACGACGACTTCGAG 60
Db 83 ATGGCCGCGTCGGATCTGGAGACCAAGGCCAAGGAGCGCTTCGTCGACGACGACTTCGAG 142
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Db 203 GCCAGCGCGCCAGGCGCACATCAAGCTCGGCAACTACACTGAGGCTGTGGCGGATGCT 262
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Qy 241 TGCATTAGCTTGAGATACCAACTGCAAGGCTCTCTGATGATGATGATGATGATGATGATGAT 300
Db 323 TGCATTAGCTTGAGATACCAACTGCAAGGCTCTCTGATGATGATGATGATGATGATGATGAT 382
Qy 301 GCATCAGCGGATCAAGGCTTGCTCTGCTATGATGATGATGATGATGATGATGATGATGATGAT 360
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Db 443 GAATCTAGCCAGGCAACAGTAAAGATGTTGAGGCTACTGTGGCTGTCTACTATTGAGGAC 502
Qy 421 AAGGAGGATTTCAAAATGAGGATACACACAGGCTGATGATGATGATGATGATGATGATGATGAT 480
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Qy 481 AAATACAGGATGATCTACTACACAGTGCACAGAGTGGTACTGACAAATATTTGCTTAAG 540
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US-10-425-114-25244
; Sequence 25244, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25244
; LENGTH: 1450
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3732-024-C2_FLI
US-10-425-114-25244
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Query Match 99.9%; Score 1084.4; DB 17; Length 1450;
Best Local Similarity 99.9%; Pred. No. 5.3e-313;
Matches 1085; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1169 TACTAA 1174

RESULT 3

US-10-425-115-18040
; Sequence 18040, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 18040
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116455C.1
US-10-425-115-18040

Query Match 99.9%; Score 1084.4; DB 18; Length 1755;
Best Local Similarity 99.9%; Pred. No. 5.8e-313;
Matches 1085; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGGCCGCTCGATCTGAGAGCAAGGCAAGAGGCTTCGTGCGACGACGACTTCGAG 60
Db 252 ATGGCCGCTCGATCTGAGAGCAAGGCAAGAGGCTTCGTGCGACGACGACTTCGAG 311
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Db 312 CTGGCCCGGAGCTTACAGCCGAGGCTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTAT 371
Qy 121 CGCGACCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 180
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RESULT 4

US-10-767-701-13951
; Sequence 13951, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

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Qy 421 AAGGAGGATTTACAAATATGAGAGATACACACAGCTGATAGAACCCCAAGCAAAACA 480
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Db 1332 TACTAA 1337

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421	AAGAGAGATTTCAAAATATGGAGAAATACACCAACAGTGTAGAAACCCCCAAAGCAAAACCA	480
519	AAGAGAGATGTCGCAATATGGATATATACACGCCAGTGGTAGAACCCCCCAAGCAAACT	578
481	AAATACAGGCATGACTTACTCAACAGATGCGCAACAGAGTGGTACTGCAATATTTGCTTAAG	540
579	AAATATAGGCATGACTACTCAACAGATGCGCAACAGAGTGGTCTCACAAATATATGCTTAAG	638
541	GGTGTTCTGCTGATAGTGTAGTCAATTGATTTGGTGAAACAGATGTTGAGTGTATCCCAAT	600
639	GGTGTTCTGCTGATAGTGTAGTCAATTGATTTGGTGATCAGATGTTGAGTGTATCCCAAT	698
601	GAAGTTCTGGTGAAGAACCATATCAATTTTCAGCCCCGTCTGTTTTCTTAAGATATCCCT	660
699	GAAGTACTTGGTGAAGAACCGTACCAATTTTCAGCCCCGTCTGTTTTCTTAAGATATCCCT	758
661	GAGAAATGCAAAATATCAAGTCTTATCCACCAAGGTTGAAATACGCTTGC AAAAGCTCGAG	720
759	GAGAAATGCAAGTATCAAGTTTTATCCACCAAGGTCGAAATACGCTTGC AAAAGCTCGAG	818
721	CAGGTGACATGGCAACACCTCGAATTTATGTGGAAGACCAAAAGACTGTTCCCGCAGAAGATA	780
819	CAGGTGACATGGCAACACCTCGAATTTATGTGGAAGACCAAAAGGCTATTTCCCGCAGAAGATA	878
781	AGCAGCGCAGCTGAAAACAGCCCCAAGACCTTCATACCCATCTTCAAGGCGAAAAGAC	840
879	AGCAGCGCAGCTGAAAACAGCCCCAAGACCTTCATACCCATCTTCAAGTCAAAAAGAC	938
841	TGGATAAACTGGAACTGGAAGTCAAAAAGGAGAGAGGAAAGAAAACCTTGATGGTGAT	900
939	TGGATAAACTGGAACTGGAAGTCAAAAAGGAGAGAGGAAAGAAAACCTTGAGAGTGAT	998
901	GCTGCATTGAAACAAATTTCTCCGTGACATCTACAAGGATGCTGATGAAGATATGCGGAGG	960
999	GCTGCATTGAAACAAAGTTCTTCCGTGATATCTACAAGGATGCTGATGAAGATATGCGGAGG	1058
961	GCCATGATGAGTCAATTCGTGGGAATCAAAATGGCACTGTTCTCTCAACCAATTTGGAAGAT	1020
1059	GCCATGAGCAAGTCAATTCAGGGAATCTAATGGTACCGTTCTCTCAACCAATTTGGAAGAT	1118
1021	GTTGGAGCAAGAGGTAGAAAGGAGCCCCCTGATGTTATGGAAGTCTCAAGAGTGGAA	1080
1119	GTTGGATCAAGAAGTGGAGAGGAGCCCTCTGATGTTATGGAAGTCTCAAGAGTGGAA	1178

RESULT 6
US-10-425-114-22598
Sequence 22598, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 22598
LENGTH: 1490
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3591-005-E5_FLI
US-10-425-114-22598

Qy	1.021	GTTGGAGCAAGAAGGTAGAAAGGAGGCCCCCTGATCGTATCGAGCTCAAGAAGTGCGAA	1080
Cb	1.197	GTTGGCTCATTACACGCTTCCTGATCGTATCGAGCTCAAGAAGTGCGAA	1246

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RESULT 7
US-10-425-115-18041
/ Sequence 18041, Application US/10425115
/ Publication NO. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 18041
/ LENGTH: 1519
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MFT4577_116456C.1
US-10-425-115-18041

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Query Match	90.0%	Score 977.6;	DB 18;	Length 1519;
Best Local Similarity	94.1%	Pred. NO. 4.7e-281;		
Matches 1016: Conservative	0;	Mismatches 64;	Indels 0;	Gaps 0;

Qy	1	ATGCCCGCTCGGACTCTGGAGACGAAGCCAAAGGAGGCGCTTGTGCGACGACGACTTCGAG	60
Db	167	ATGCCCCGCTCGGACTCTGGAGACGAAGCCAAAGGAGGCGCTTGTGCGACGACGACTTCGAG	226
Qy	61	CTGGCCACCGGAGCTTACAGCCAGGCCATCGACCGCGGGCCGCCACCGCCGACCTCTAT	120
Db	227	CTGGCCCGCGAACTCTACACGACGGCCATCGACCGCGGGCCGCCACCTGCCGATCTCTAC	286
Qy	121	GCCGACCGCGCCGAGGCCACATCAAGCTCGGCAACTACACTGAGGCTGTGCGGATGCT	180
Db	287	GCCGACCGCGCCGAGGCCACATCAAGCTCGGCAACTACACTGAGGCTGTGCGGATGCT	346
Qy	181	AACAAAGCAATTGAGCTTGATCTCTATGATGCAATAAGCTTACTACCGGAAGGTCCTGCA	240
Db	347	AACAAAGCAATTGCTTCTGATCCTCAATGCAATAAGGCTTACTACCGGAAGGTCCTGCA	406
Qy	241	TGCATTAGCTTTGAGAAATACCAACTCGAAGGCTGCTCTTGTAGTTGGGTTCTTCTTAT	300
Db	407	TGCATTAGCTTTGAGAAATACCAACTCGAAGGCTGCTCTTGTAGTTAGTTCTTCTTAT	466
Qy	301	GCATCAGCGGATTCAGAGTTTTCCTCGTCTATTGAAAGGAATGTGATGAGCGCATTCGCTGAG	360
Db	467	GCATCAGCGGATTCAGAGTTTTCCTCGTCTATTGAAAGGAATGTGATGAGCGCATTCGCTGAG	526
Qy	361	GAATCTAGCCAGGCACAGTAAGAAATGTTGAGGCTACTGTGCGCTGCTACTATTGAGGAC	420
Db	527	GAATCTAGCCAGGCACAGTAAGAAATGTCGAGGCTCTGTAGCTGCTACTGTGTGAGGAC	586
Qy	421	RAGGAGGATTTCCACAAATATGAGAAATACACACAGTATAGAACCCGCCAAGCAACCA	480
Db	587	RAGGAGGATTTCCGCAAAATATGAGAAATACACCGCCAGTGTAGAACCCGCCAAGCAACCT	646
Qy	481	AAATACAGGCATGACTACTACAACTGAGGCGCCACAGAAAGTGGTACTGCAATATTTGCTAAG	540
Db	647	AAATATAGCATGACTACTACAACTGAGGCGCCACAGAAAGTGGTACTGCAATATATGCTAAG	706
Qy	541	GGTGTTCTTCGCTGATAGTGTAGTCAATGTTTGGTGAACAGATGTTGAGTGTATCCATT	600
Db	707	GGTGTGTTCTTCGCTGATAGTGTAGTCAATGTTTGGTGAACAGATGTTGAGTGTATCCATT	766
Qy	601	GAGTCTTCCTGGTGAAGAAACATACCACTATTTTCAGCCCCGCTCTGTGTTTCTAAGATATATCCCT	660

RESULT 8

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US-10-425-114-24871
/ Sequence 24871, Application US/10425114
/ Publication No. US20040034988A1
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E.
/ APPLICANT: Cao, Yongwei
/
/ TITLE OF INVENTION: Nucleic Acid Molec
/ TITLE OF INVENTION: Plants and Uses T
/
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,
/ CURRENT FILING DATE: 2003-04-28
/
/ NUMBER OF SEQ ID NOS: 73128
/
/ SEQ ID NO 24871
/
/ LENGTH: 1649
/
/ TYPE: DNA
/ ORGANISM: Zea mays
/
/ FEATURE:
/
/ OTHER INFORMATION: Clone ID: LIB3689-
/
US-10-425-114-24871

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		Query Match	79.4%;	Score 862;	DB 17;	Length 1649;
		Best Local Similarity	83.5%;	Pred. No. 1.8e-246;		
		Matches 1086; Conservative	0;	Mismatches 0;	Indels 214;	Gaps 1;
Qy	1	ATGGCCGCGTCGAGTCTGGAGACCAAGGCCAAGAGGCCTTCGTGCACGACGA	CTTCGAG	60		
Dd	91	ATGGCCGCGTCGAGTCTGGAGACCAAGGCCAAGAGGCCTTCGTGCACGACGA	CTTCGAG	150		
Qy	61	CTGGCCACCAGACTCTACAGCACCAGGCATCGACGCCGGGCCCGGCCACCGCGCACCTCTAT		120		
Dd	151	CTGGCCACCAGACTCTACAGCACCAGGCATCGACGCCGGGCCCGGCCACCGCGCACCTCTAT		210		
Qy	121	GCCGACCCGCGCCAGGGCGCATCAAGCTCGGCNACTACA	CTGAGGCTGTGGCGGATGCT	180		
Dd	211	GCCGACCCGCGCCAGGGCGCATCAAGCTCGGCNACTACA	CTGAGGCTGTGGCGGATGCT	270		

767	DB		GAAGTACCTGGTGAAGAACCGTACATTTTCAGCCCGCTCTGTTTCTAAGATTATCCCT	826
661	QY		GAGAAATGCAATATCAAAGTCTTATTCACCAAGTTGAATACGCTTGCCTTGCATAAGCTGAG	720
827	DB		GAGAAATGCAAGTATCAAGTTTATTCACCAAGTGCATAACGCTTGCCTTGCATAAGCTGAG	886
721	QY		CAGGTGACATGGACAAACCTCGATTATAGTGAAGACCAAGACCTCTTCCCCACAGAGATA	780
887	DB		CAGGTGACATGGACAAACCTCGATTATAGTGAAGACCAAGACCTATCCCCACAGAGATA	946
781	QY		AGCAGCCAGCTGAACACAGCCCCAGACCTTCATACCCATCTTCAAGGCGCAAAAAGAC	840
947	DB		AGCAGCCAGCTGAACACAGCCCCAGACCTTCATACCCATCTTCAAGTCAAAAAGGAC	1006
841	QY		TGGGATTAACTCGAAAGCTGAAGTCAAAAAGGAGGAGGAAGAAAACTTGATGTGAT	900
1007	DB		TGGGATTAACTCGAAAGCTGAAGTAAAAAAGGAGGAGGAAGAAAACTTGATGTGAT	1066
901	QY		GCTGCATTTGAACAAATTTCTTCGGTGACATCTCAAGGATGCTGATGAAGATATCCGAGG	960
1067	DB		GCTGCATTTGAACAAATTTCTTCGGTGATATCTCAAGGATGCTGATGAAGATATCCGAGG	1126
961	QY		GCCATGATGAAGTCAATTCGTGGAAATCAATGGCACGTCTCTCAACCAATTCGAAAGAT	1020
1127	DB		GCCATGACAAAGTCAATTCAGGGAATCTAATGGTACCGTTCTCTCAACCAATTCGAAAGAT	1186
1021	QY		GTTCGAGCAAGAGGTAGACGGAGCCCCCTGATGGTATGGAGCTCAAGAGCTGGAA	1080
1187	DB		GTTCGATCAAGACGGTGGAGCGAGCCCTCTCGATGGTATGGAGCTCAAGAGCTGGAA	1246

Qy	181	AACAAAGCAATTGAGCTTGATCCTATGATGCATAAAGCTTTACTACGGAAAGGTGCTGCA	241
Db	271	AACAAAGCAATTGAGCTTGATCCTATGATGCATAAAGCTTTACTACGGAAAGGTGCTGCA	330
Qy	241	TGCATTAAAGCTTGAAGAAATACCAACTGCAAGGCTGCTCTTGAGTTGGTTCTTCTTAT	300
Db	331	TGCATTAAAGCTTGAAGAAATACCAAACTGCAAAAGGCTGCTCTTGAGTTGGTTCTTCTTAT	390
Qy	301	GCATCAGCGGATTCAGGTTTTCCTCGTCTATTGAAAGGAATGTGATGAGCGCATCGCT---	357
Db	391	GCATCAGCGGATTCAGGTTTTCCTCGTCTATTGAAAGGAATGTGATGAGCGCATCGCTGTT	450
Qy	358	-----	357
Db	451	GAGAAAAATTAACCTTCAGCAGTGTGTGTATCTCGTGGTGGTTGGGGCTTCCTGGGTAT	510
Qy	358	-----	357
Db	511	GCAATGTGGTGATGCTATTTTCTGACGATATGAGTCCATTTAGCTGCTTTCCTTGAGAA	570
Qy	358	-----	357
Db	571	ATGTTTGTAGCAGCCTTGTAGACTGGGGATGATTATGTTTTCAGCTTAATCATCTCATAC	630
Qy	358	-----	386
Db	631	TACCTGTCAATATTTTGTATTATGTTTCCAGAGGAATCTTAGCCAGGCACCAAGTAAAGAA	690
Qy	387	TGTTGAGGCTACTGCGGCTGCTACTATTGAGGACAAAGAGGATTTTCAAAATATGGAGAA	446
Db	691	TGTTGAGGCTACTGCGGCTGCTACTATTGAGGACAAAGAGGATTTTCAAAATATGGAGAA	750
Qy	447	TACACCACAGTGATAGAAACCCCAAGCAAAACCAAAATACAGGCATGACTACTCAACAG	506
Db	751	TACACCACAGTGATAGAAACCCCAAGCAAAACCAAAATACAGGCATGACTACTCAACAG	810
Qy	507	TGCCACAGAAAGTGTPACTGCAAAATATTTGCTAAAGGGTGTCTCTGCTGATAGTGTAGTCA	566
Db	811	TGCCACAGAAAGTGTPACTGCAAAATATTTGCTAAAGGGTGTCTCTGCTGATGTAGTGTAT	870
Qy	567	TGATTTTGGTGAAACAGATGTTGAGTGATCATATTGAAAGTTTCTGCTGATAGTGTAGTCA	626
Db	871	TGATTTTGGTGAAACAGATGTTGAGTGATCATATTGAAAGTTTCTGCTGATAGTGTAGTCA	930
Qy	627	TTTTCAGCCCGCTGTGTTTCTAAGATTATCCCTGAGAAATGCAAAATATCAAGTCTTATC	686
Db	931	TTTTCAGCCCGCTGTGTTTCTAAGATTATCCCTGAGAAATGCAAAATATCAAGTCTTATC	990
Qy	687	CACCAAGTTGAAATACGCCCTTGCAAAAGCTGAGCAGTGACATGGACAACCCCTGGATTA	746
Db	991	CACCAAGTTGAAATACGCCCTTGCAAAAGCTGAGCAGTGACATGGACAACCCCTGGATTA	1050
Qy	747	TAGTGGAAAGACCAAGACTGTTCCGAGAAATAGCACGCCAGCTGAAAACAGCCCCAAG	806
Db	1051	TAGTGGAAAGACCAAGACTGTTCCGAGAAATAGCACGCCAGCTGAAAACAGCCCCAAG	1110
Qy	807	ACCTTCATACCCATCTTCARAGGCGAATAAGACTGGGATAACTGGAGAGCTGAAGTCAA	866
Db	1111	ACCTTCATACCCATCTTCARAGGCGAATAAGACTGGGATAACTGGAGAGCTGAAGTCAA	1170
Qy	867	AAAGGAGGAGGAAGGAAGAAATCTTGATGTGATGCTGCAATTGAACAAATTTCTCCGTGA	926
Db	1171	AAAGGAGGAGGAAGGAAGAAATCTTGATGTGATGCTGCAATTGAACAAATTTCTCCGTGA	1230
Qy	927	CATCTACAAGGATGCTGATGAAGATATGCGGAGGCGCATGATGAAGTCAATTCGTGGAATC	986
Db	1231	CATCTACAAGGATGCTGATGAAGATATGCGGAGGCGCATGATGAAGTCAATTCGTGGAATC	1290
Qy	987	AAATGGCACATGTTCTCTCAACCAATTCGAAGATGTTGGACCAAGAGGTAGAGGGAG	1046
Db	1291	AAATGGCACATGTTCTCTCAACCAATTCGAAGATGTTGGACCAAGAGGTAGAGGGAG	1350
Qy	1047	CCCCCTGATGTTATGGAGCTCAAGAAAGTGGGAATACTAA	1086

Db	1351	CCCCCTGATGGTATGGAGCTCAAGAAATGGGAATACTAA	1390
RESULT 9			
US-10-425-115-18039			
; Sequence 18039, Application US/10425115			
; Publication No. US20040214272A1			
; GENERAL INFORMATION:			
; APPLICANT: La Rosa, Thomas J.			
; APPLICANT: Kowalic, David K.			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Mol			
; FILE REFERENCE: 38-21(53222)B			
; CURRENT APPLICATION NUMBER: US/10/425,115			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 369326			
; SEQ ID NO 18039			
; LENGTH: 1706			
; TYPE: DNA			
; ORGANISM: Zea mays			
; FEATURE:			
; OTHER INFORMATION: Clone ID: MRT4577_116454C.1			
US-10-425-115-18039			
Query Match 79.4%; Score 862; DB 18; Length			
Best Local Similarity 83.5%; Pred. No. 1.9e-246;			
Matches 1086; Conservative 0; Mismatches 0; Inde			
Qy	1	ATGCCCGCTCGGATCTGGAGAGCAAGGCCAAGGAGGCGCTTCGTGTC	
Db	91	ATGCCCGCTCGGATCTGGAGAGCAAGGCCAAGGAGGCGCTTCGTGTC	
Qy	61	CTGSCCAACCGAGCTCTACGCCAGGCCATCGACGCCGGGCCCGCCGC	
Db	151	CTGSCCAACCGAGCTCTACGCCAGGCCATCGACGCCGGGCCCGCCGC	
Qy	121	GCCGACCGGCCCGCAGGCGCATCAAGCTCGGCAACTACACTGAGAG	
Db	211	GCCGACCGGCCCGCAGGCGCATCAAGCTCGGCAACTACACTGAGAG	
Qy	181	AACAAAGCAATTGAGCTTTGATCTCTATGATGCTATAAAGCTTTACTAC	
Db	271	AACAAAGCAATTGAGCTTTGATCTCTATGATGCTATAAAGCTTTACTAC	
Qy	241	TGCATTAAGCTTGAAGAATACCAAACTGCAAAAGGCTGCTCTTGAGT	
Db	331	TGCATTAAGCTTGAAGAATACCAAACTGCAAAAGGCTGCTCTTGAGT	
Qy	301	GCATCAGCGGATTCAGGTTTGTGCTCTATTGAAGGAATGTGAT	
Db	391	GCATCAGCGGATTCAGGTTTGTGCTCTATTGAAGGAATGTGAT	
Qy	358	-----	
Db	451	GAGAAAAATTAACTTCAGCAGTGTGTGTATCTGCTGGTGGTGT	
Qy	358	-----	
Db	511	GCAATGTGTGCATGCTATTTCTGACGATATGAGTCCACTTAGCT	
Qy	358	-----	
Db	571	ATGTTTGTAGCAGCTTGTAGACTGGGGGATGATTATGTTTCAGCT	
Qy	358	-----	
Db	631	TACCTGTCAATGTTATTTTGTATTGTTTCCAGAGGAATCTAGCCAG	
Qy	387	TGTTGAGGCTACTGTGCGCTGCTACTATTTCAGGACAGGAGGATTTCT	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 20, 2005, 18:28:41 ; Search time 134 Seconds
(without alignments)
895.417 Million cell updates/sec

Title: US-10-609-078-8.
Perfect score: 1861
Sequence: 1 MAADLESKAEAFVDDDFE.....GAKVSGSPDGMLKKWEY 361

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1861	100.0	388	15	US-10-425-114-61162
2	1861	100.0	390	15	US-10-425-114-61204
3	1771.5	95.2	395	16	US-10-767-701-45515
4	1740	93.5	393	15	US-10-425-114-61212
5	1740	93.5	416	15	US-10-425-114-65836
6	1578	84.8	376	16	US-10-437-963-139712
7	1263	67.9	256	15	US-10-425-114-61200
8	1176.5	63.2	357	15	US-10-424-599-224769
9	1146.5	61.6	359	15	US-10-424-599-208541
10	925.5	49.7	357	15	US-10-424-599-241114
11	729	39.2	160	15	US-10-424-599-261373
12	615	33.0	344	15	US-10-264-049-3093
13	603.5	32.4	223	16	US-10-437-963-146392

14	599	32.2	168	15	US-10-424-599-224775	Sequence 224775,
15	594	31.9	365	14	US-10-287-218-12	Sequence 12, Appl
16	594	31.9	365	16	US-10-474-291-12	Sequence 12, Appl
17	471	25.3	229	16	US-10-437-963-146382	Sequence 146382,
18	464	24.9	196	10	US-09-983-802-393	Sequence 393, App
19	464	24.9	196	10	US-09-984-490-393	Sequence 393, App
20	464	24.9	196	11	US-09-973-278-503	Sequence 503, App
21	464	24.9	228	10	US-09-983-802-401	Sequence 401, App
22	464	24.9	228	10	US-09-984-490-401	Sequence 401, App
23	464	24.9	228	11	US-09-973-278-511	Sequence 511, App
24	445	23.8	123	15	US-10-032-585-7066	Sequence 7066, Ap
25	445	23.8	123	14	US-10-424-599-241112	Sequence 241112,
26	405	21.8	400	14	US-10-128-714-3417	Sequence 3417, Ap
27	403	21.7	123	15	US-10-424-599-18698	Sequence 18698,
28	383	20.6	478	14	US-10-128-714-8417	Sequence 8417, Ap
29	239	12.8	82	15	US-10-424-599-192478	Sequence 192478,
30	235.5	12.7	483	16	US-10-437-963-195520	Sequence 195520,
31	226.5	12.2	482	15	US-10-424-599-191442	Sequence 191442,
32	224	12.0	482	14	US-10-298-638-27	Sequence 27, Appl
33	224	12.0	485	14	US-10-298-638-10	Sequence 28, Appl
34	223	12.0	533	14	US-10-767-701-41397	Sequence 41397, A
35	219.5	11.8	163	16	US-10-425-114-61206	Sequence 61206, A
36	219.5	11.8	488	15	US-10-424-599-183984	Sequence 183984,
37	213	11.4	101	15	US-09-991-496-127	Sequence 127, App
38	203.5	10.9	955	9	US-09-874-923-97	Sequence 97, Appl
39	197.5	10.6	1427	9	US-09-991-496-97	Sequence 97, Appl
40	197.5	10.6	1427	9	US-09-874-923-96	Sequence 96, Appl
41	197.5	10.6	1641	9	US-09-991-496-96	Sequence 296, App
42	197.5	10.6	1641	9	US-10-043-487-296	Sequence 55003, A
43	192	10.3	494	14	US-10-425-114-55903	Sequence 35628, A
44	190	10.2	590	15	US-10-767-701-35628	
45	186	10.0	191	16		

ALIGNMENTS

RESULT 1

US-10-425-114-61162
; Sequence 61162, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 61162
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3059-061-D10_FLI.pep
US-10-425-114-61162

Query Match 100.0%; Score 1861; DB 15; Length 388;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAADLESKAEAFVDDDFELATLYSCAIDAGPATADLYADRAQAHLKLGNYTEAVADA	60
DB	28	MAADLESKAEAFVDDDFELATLYSCAIDAGPATADLYADRAQAHLKLGNYTEAVADA	87
QY	61	NKATELDPMMHKAYYRKGAAACIKLEEVQTAKAALGLSSVSGSRFARLLKCEDERIAE	120
DB	88	NKATELDPMMHKAYYRKGAAACIKLEEVQTAKAALGLSSVSGSRFARLLKCEDERIAE	147

APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 61212
LENGTH: 393
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3960-013-B4_FLI.pep
US-10-425-114-61212

Query Match 93.5%; Score 1740; DB 15; Length 393;
Best Local Similarity 93.1%; Pred. No. 9.3e-128;
Matches 335; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
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Db 33 MAASDLESKAKEAFVDDDFELAAELYTQADAGPATADLYADRAQAHIKLGNYTEAVADA 92
Qy 61 NKAELDPMHKAAYRKGAAACIKLEEQYAKAALGSSYASGDSRFRLLKCEDEIAE 120
Db 93 NKAIGLDPTHKAYRKGAAACIKLEEQYAKAALGSSYAPGDSRFRLLKCEDEIAE 152
Qy 121 ESSQAPKVNVEATVAETIEDKEDFTNMNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 180
Db 153 ESSQAPKVNVEATVAETIEDKEDVANNDNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 212
Qy 181 GVPADSVVDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRLAKAE 240
Db 213 GVPADSVVDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRLAKAE 272
Qy 241 QVTWTTLDYSGRPKTPQKISTPAETAPRPSYSSKAKDMDKLEAEVKKKEEKLGD 300
Db 273 QVTWTTLDYSGRPKTPQKISTPAETAPRPSYSSKAKDMDKLEAEVKKKEEKLGD 332
Qy 301 AALNKFRIYKDADMRAMKSFVESNGTVLSTNWKDVGAKYVGGSPDGMELKKWE 360
Db 333 AALNKFRIYKDADMRAMKSFRESNGTVLSTNWKDVGSKTVEASPPDGMELKKWE 392

RESULT 5
US-10-425-114-65836
Sequence 65836, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 65836
LENGTH: 416
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3591-005-55_FLI.pep
US-10-425-114-65836

Query Match 93.5%; Score 1740; DB 15; Length 416;

Best Local Similarity 93.1%; Pred. No. 1e-127;
Matches 335; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
Qy 1 MAASDLESKAKEAFVDDDFELATLYSOAIDAGPATADLYADRAQAHIKLGNYTEAVADA 60
Db 56 MAASDLESKAKEAFVDDDFELAAELYTQADAGPATADLYADRAQAHIKLGNYTEAVADA 115
Qy 61 NKAELDPMHKAAYRKGAAACIKLEEQYAKAALGSSYASGDSRFRLLKCEDEIAE 120
Db 116 NKAIGLDPTHKAYRKGAAACIKLEEQYAKAALGSSYAPGDSRFRLLKCEDEIAE 175
Qy 121 ESSQAPKVNVEATVAETIEDKEDFTNMNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 180
Db 176 ESSQAPKVNVEATVAETIEDKEDVANNDNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 235
Qy 181 GVPADSVVDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRLAKAE 240
Db 236 GVPADSVVDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRLAKAE 295
Qy 241 QVTWTTLDYSGRPKTPQKISTPAETAPRPSYSSKAKDMDKLEAEVKKKEEKLGD 300
Db 296 QVTWTTLDYSGRPKTPQKISTPAETAPRPSYSSKAKDMDKLEAEVKKKEEKLGD 355
Qy 301 AALNKFRIYKDADMRAMKSFVESNGTVLSTNWKDVGAKYVGGSPDGMELKKWE 360
Db 356 AALNKFRIYKDADMRAMKSFRESNGTVLSTNWKDVGSKTVEASPPDGMELKKWE 415

RESULT 6
US-10-437-963-139712
Sequence 139712, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 139712
LENGTH: 376
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_40977C.1.pap
US-10-437-963-139712

Query Match 84.8%; Score 1578; DB 16; Length 376;
Best Local Similarity 82.1%; Pred. No. 4.2e-115;
Matches 307; Conservative 27; Mismatches 24; Indels 16; Gaps 3;
Qy 2 AASDLESKAKEAFVDDDFELATLYSOAIDAGPATADLYADRAQAHIKLGNYTEAVADA 61
Db 5 AASDLESKAKEAFVDDDFELAAELYTQAEASPATRELYADRAQAHIKLGNYTEAVADA 64
Qy 62 KAIELDPMHKAAYRKGAAACIKLEEQYAKAALGSSYASGDSRFRLLKCEDEIAE 121
Db 65 KAIELDPMHKAAYRKGAAACIKLEEQYAKAALGSSYASGDSRFRLLKCEDEIAE 124
Qy 122 SSQAPKVNVEATVAETIEDKEDFTNMNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 176
Db 125 LSEVPVTKAEDGAAAPSVASFVEEKDDAANNMDNTPPMVE--VKPKYRHDYNSATEVVLTIYAK 182
Qy 177 IFAGKVPADSVVDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRL 236

Db 183 IPAKGVPAENVVDFGEQMLSVSIEVPGEEYHFQPRLFPSKIIPKSRQYVLSTKVEIRL 242
 QY 237 AKAEQVTTWTLTLDYSGRPKTVPOKISTP-----AETAPRPSVPSSKAKKDWKLEAE 287
 Db 243 AKAEQVTTWTLTLDYSGRPKTVPOKISTP-----AETAPRPSVPSSKAKKDWKLEAE 302
 QY 288 VKKEEKEKLDGDAALNKFPRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVE 347
 Db 303 VKKEEKEKLDGDAALNKFPRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVE 362
 QY 348 GSPDPGMELKKWEY 361
 Db 363 GSPDPGMELKKWEY 376

RESULT 7

US-10-425-114-61200
 ; Sequence 61200, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 61200
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3689-210-C7_FLI.pep
 US-10-425-114-61200

Query Match 67.9%; Score 1263; DB 15; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.1e-90;
 Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 120 BESSQAPKVNVEATVAATIEDKEDFTNMTPPPVIEPPSKYRHDYNSATEVVLTF 179
 Db 15 BESSQAPKVNVEATVAATIEDKEDFTNMTPPPVIEPPSKYRHDYNSATEVVLTF 74
 QY 180 KGVPADSVVIDFGEQMLSVSIEVPGEEYHFQPRLFPSKIIPKSRQYVLSTKVEIRLAK 239
 Db 75 KGVPADSVVIDFGEQMLSVSIEVPGEEYHFQPRLFPSKIIPKSRQYVLSTKVEIRLAK 134
 QY 240 EQVTTWTLTLDYSGRPKTVPOKISTPABTAPRPSVPSSKAKKDWKLEAEVKKKEEKL 299
 Db 135 EQVTTWTLTLDYSGRPKTVPOKISTPABTAPRPSVPSSKAKKDWKLEAEVKKKEEKL 194
 QY 300 DAALNKFPRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVEGSPDGMELKK 359
 Db 195 DAALNKFPRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVEGSPDGMELKK 254
 QY 360 EY 361
 Db 255 EY 256

RESULT 8

US-10-424-599-224769
 ; Sequence 224769, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 224769
 ; LENGTH: 357
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(357)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_44998C.1.pep
 US-10-424-599-224769

Query Match 63.2%; Score 1176.5; DB 15; Length 357;
 Best Local Similarity 64.5%; Pred. No. 1e-83;
 Matches 234; Conservative 48; Mismatches 68; Indels 13; Gaps 6;
 QY 3 ASDLESKAKGAFVDDDFELATYLSQADPATADLYADRAQAHIKLGNYTEAVADANK 62
 Db 2 ASDLELKAKGAFEDDNDYDLATLQAIGLSPNNADLYADRAQVNIKVNLLTEAVSDANK 61
 QY 63 AIELDPMHKKAYKRGACIKLEEVOTAKALELGSYASGDSRFARLLKCEDRIAEES 122
 Db 62 AIELNPSHKKAYLRKGTACIKLEEVOTAKALELGSYASGDSRFARLLKCEDRIAEES 121
 QY 123 SQAPVQVVEATVAATIEDKEDFTNMTPPPVIEPPS-----KPKYRHDYNSATEVVLTF 178
 Db 122 GVPIQESITQGAATRAVE-----AENDLP--EPTVTWVKPYRHEFYQKPDENVITIF 175
 QY 179 AKGVPADSVVIDFGEQMLSVSIEVPGEEYHFQPRLFPSKIIPKSRQYVLSTKVEIRLAK 238
 Db 176 AKGIFRDSITVDFGEQILSVTINIPCKDAYVFPQPRLFPSKIIPKSRQYVLSTKVEIRLAK 235
 QY 239 AEQVTTWTLTLDYSGRPKTVPOKIST-PAETAPRPSVPSSKAKK-DWDKLEAEVKKKEEK 296
 Db 236 ADHLQWTSLEFN-KGSTVAQRFSVLPVARGEKPTIPSSKPKKXKDWKLEAQVKKKEEK 294
 QY 297 LDGDAALNKFPRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVEGSPDGMEL 356
 Db 295 LDGDAALNKFPRDIYQDADSDTRAMSKSFVESNGTVLSTNNKDVGAKKVEGSPDGMEL 354
 QY 357 KKW 359
 Db 355 KKW 357

RESULT 9

US-10-424-599-208541
 ; Sequence 208541, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 208541
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_30341C.1.pep

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 23, 2005, 00:00:36 ; Search time 3903.36 Seconds
(without alignments)
10590.311 Million cell updates/sec

Title: US-10-609-078-9
Perfect score: 1086
Sequence: 1 atggcgctgcgatctgga.....tcaagaagtggaataactaa 1086

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:.*
2: gb_est2:.*
3: gb_hic:.*
4: gb_est3:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_gss1:.*
9: gb_gss2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1068.4	98.4	1646	3	AY103953 Zea mays
2	698.2	64.3	1131	9	CL959360 OeIFCC002
3	652.4	60.1	668	2	AW076274 614063D11
4	650.2	59.9	752	6	CD443320 EL01N0424
5	647	59.6	756	6	CA184150 SCRFST314
6	643.4	59.2	659	2	AW090936 614068G07
7	643.4	59.2	772	6	CA258233 SCCRT300
8	641	59.0	759	6	CA245820 SCEZF508
9	631	58.1	666	6	CA215140 SCSBAD112
10	608.2	56.0	678	6	CA177070 SMCST105
11	607	55.9	665	6	CA153735 SCVPR2203
12	596.4	54.9	622	6	CA229980 SCUFPL3C0
13	583.4	53.7	586	2	AW042392 614028B03
14	583.4	53.7	609	6	CA229238 SCAGFL302
15	572	52.7	702	6	CA262995 SCPRLB202
16	566	52.1	718	6	CA106435 SCQHR101
17	565.2	52.0	594	6	CA098274 SMCCL605
18	562	51.7	574	4	B1644145 949022C08
19	557.2	51.3	630	6	CA486265 WHE4329 D
20	555.6	51.2	579	2	AW066518 660015G08
21	552.8	50.9	680	6	CA128103 SCAGLR203
22	550	50.6	550	4	B1679413 949001E02
23	550	50.6	914	6	CA084222 SCEQAW203
24	545	50.2	588	5	BU499669 946178B11

25	541	49.8	601	6	CA176126
26	535.8	49.3	553	5	BU098322
27	529.4	48.7	612	6	CA234143 SCCCL6C0
28	523	48.2	615	6	CA283412 SCSBSD105
29	522.6	48.1	730	2	BE362001 DGI 83 H0
30	520.8	48.0	725	6	CA094787 SCCCL401
31	520	47.9	578	6	CD996630 QSC6A07.X
32	519.6	47.8	708	6	CA240596 SCSBFL406
33	514.8	47.4	1089	7	CK208966 FGAS02069
34	512.2	47.2	693	6	CA104899 SCJFHR1C0
35	511.6	47.1	606	6	CA083869 SCEPAM205
36	508.4	46.8	625	6	CA266503 SCAGLB204
37	507.4	46.7	518	2	AW057009 66007D01
38	507.4	46.7	862	6	CB655564 OSUNBC09B
39	507.2	46.7	652	6	CA102017 SCAGHR101
40	505.2	46.5	798	6	CA176210 SCJLST102
41	500.6	46.1	610	6	CA184034 SCQST311
42	499.4	46.0	643	6	CA251380 SCQSPFL112
43	498.8	45.9	778	6	CA227695 SCJLFL301
44	498.4	45.9	607	6	CA120629 SCCCLR108
45	487.4	44.9	792	6	CB657723 OSJNEC13E

ALIGNMENTS

RESULT 1
LOCUS AY103953 1646 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PC0098564 mRNA sequence.
ACCESSION AY103953
VERSION AY103953.1 GI:21207031
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 1646)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1646)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES
Location/Qualifiers
1..1646
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:635643"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 98.4%; Score 1068.4; DB 3; Length 1646;

Db 1221 GTTGGAGCAAGAAGGTAGAGGGAGGCCCCCTGATGTTATGGAGCTCAAGAAGTGGAA 128

QY 1081 TACTAA 1086
|||||

Db 1281 TACTAA 1286

RESULT 2

CL959360

LOCUS OsIFCC002721 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. GSS 21-SEP-2004

DEFINITION

ACCESSION CL959360

VERSION CL959360.1 GI:52373436

KEYWORDS GSS.

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)

REFERENCE Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriarhatoideae; Oryzoideae; Oryza.

AUTHORS 1 (bases 1 to 1131)

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.

TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

JOURNAL Unpublished (2004)

COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

FEATURES

source

1..1131
Location/Qualifiers

1. ..1131
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 64.3%; Score 698.2; DB 9; Length 1131;
Best Local Similarity 79.0%; Pred. No. 1.8e-184;
Matches 899; Conservative 0; Mismatches 188; Indels 48; Gaps 3;

QY 4 GCCTGGTGGATCTGAGAGCAAGCCCAAGGAGGCTTCGTCGACGACGACTTCGAGCTG 63

Db 13 GCCTGGTGGATCTGAGAGCAAGCCCAAGGAGGCTTCGTCGACGACGACTTCGAGCTG 72

QY 64 GCACCGAGCTCTACAGCCAGGCCATCGACGCGCGCGCCGCCACCGCGACCTCTATGCC 123

Db 73 GCCTGGAGCTCTACCGAGGCAATCGAGGCGAGCCCGCCCGCCGCGAGCTCTACGCC 132

QY 124 GACCGCGCCCGAGCGCACATCAAGCTCGGCACATCACTGAGGCTGTGGCGGATGCTAAC 183

Db 133 GACCGCGCCCGAGCGCCATATCAAGCTAGGCACTACCTGAGGCTGTAGCTGATGCTAAC 192

QY 184 AAGCAATGAGCTTGATCTATGATGATTAAGCTTACTACCGGAAAGGTGCTCATGC 243

Db 193 AAGCCATGAGCTTGATCTATGATGATTAAGCTTACTACCGGAAAGGTGCTCATGC 252

QY 244 ATTAGCTTGAAGATACAAACTGCAAGGCTGCTTTGAGTTGGGTTCTTTATGCA 303

Db 253 ATACGACTGGAGGAGTATCAAACTGCAAAAGCGGCTCTTGAATTTGGGTTACTCGTTGCA 312

QY 304 TCAGCGGATCAAGGTTTGCTCGTCTATTGTAAGGAATGTGATGAGCGCATCGCTGAGGAA 363

Db 313 TCTGTGACTCAAGTTTACTCGCTTAATGAAGGATGTGATGAGGCATTTGCTGAGGAG 372

364	TCCTAGCCGACCACTAAGATGTTGAGG	-----CTACTGTGCGTCTGCT	408
373	CTTAGTGAAGTCCCTGTTTAAAGAGGCTCAAGATGGAGCAGCTGCGCCCTCTGTGTTGCTTTCT		432
409	ACTATTGAGGCAAGAGGAGGATTTTACAAATATGGAGAATACACACCAGTGTATGAACACC		468
433	TTTGTGTAGGAAAAGGATGCTGCAACATGGATATACACCAACCAATGGTAGA	----	488
469	CCAAGCAAAACAAAATACAGGATGACTATCAACACAGTGCACAGAAAGTGGTACTGACA		528
489	--AGTGAAGCCAAAATACAGGACGAGCTTCTACAAACAGTGTCTACAGAAAGTTGTTATTGACA		546
529	ATATTTGCTAAGGGTGTTCCTGCTGATAGTGTAGTCTATTGATTTTGGTGAACAGATGTTG		588
547	ATTTTTCGAAAGGGTGTTCCTGCTGAGAAATGTTGTGTGTAATTTTGGTGAACAAATGTTA		606
589	AGTGTATCCATTGAAGTTTCTGTGTGAAGAAACCATACCAATTTTCAGCCCGCTGTGTTTTCT		648
607	AGTGTGTGATTGAAGTCCCTGGAGAGGAGCGGTACCAATTTTCAGCCTCGTCTGTTTTCT		666
649	AAGATTATCCCTGAGAAATGCAAAATATCAAGTCTTTATCCACAAAGTTTGAATACGCGTT		708
667	AAGATCATCCTCGAGAAAAGCAGATACCAAGTGTCTATCCAGAAAGTTTGAATTAAGACTG		726
709	GCAAAAGCTGAGCAGGTGACATGACCAACCTGGAATTTATAGTGAAGACCAAGACGTGTT		768
727	GCTAAAGCTGAACAGATTACATGAGCCTCACTTGATTTATGATATAAACCAAAAGGCTGTT		786
769	CCCACAGAAGATTAAGCAGC	-----CAGCTGAAACAGCC	801
787	CCACAAAGATATCCCTCAGTTTTACTGATAGCCCTCTTTTATCAGCTGAATCGGCC		846
802	CCAAGACCTTCATCCCATCTTCAAGGCGAAAAAGACTGGGATAAATGGAAGCTGAA		861
847	CAGAGGCCATCATATCCTTCTCTCAAAATCCAAGAAAGACTGGGATAAATCGGAAGCTGAA		906
862	GTCAAAGAGGAGGAGGAAGAAACTTGATGCTGATGCTGCATGTGAACAAATCTTTC		921
907	GTTAAAAGGAGGAGGAGGAGAGAGCGCTTGAAGCGATGCTGCTGATTTGAACAAATTTTC		966
922	CGTGACATCTACAAGGATGCTGATGAAGATATCGGAGGGCCATGATGAAGTCAATCGTG		981
967	CGTGACATCTACAGTATGCTGATGAAGACATGCGCAGCAATGATGAATCTTTTGT		1026
982	GAATCAAAATGGCACTGTTTCTCTCAACCAATTTGGAAGATGTTGGAGCAAAAGAGGTAGAA		1041
1027	GAATCTAAACGCTACTGTTCTGTGCGACCAATTGGAAGATGTTGCTCGAAGAGGTAGAG		1086
1042	GGAGAGCCCCCTGATGATGTAATGGAGCTCAAGAGTGGGAATACTAA		1086
1087	GGAAGCCCACTGATGGGATGGAGCTTAAGAAATGGGAGTACTAA		1131

RESULT 3	AW076274	LOCUS	AW076274	DEFINITION	614053D11.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA, mRNA sequence.	668 bp mRNA linear EST 14-OCT-1999
ACCESSION	AW076274	VERSION	AW076274.1	GI:6031267		
KEYWORDS	EST.	SOURCE	Zea mays			
ORGANISM	Zea mays					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					
AUTHORS	1 (bases 1 to 668)					
TITLE	Walbot.V.					
JOURNAL	Maize ESTs from various cDNA libraries sequenced at Stanford University					
COMMENT	Unpublished (1999) Contact: Walbot V Department of Biological Sciences					

Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614063 row: D column: 11.
Location/Qualifiers
1. .868
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W23"
/db_xref="taxon:4577"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOUR"
/clone_lib="614 - root cDNA library from Walbot Lab"
/note="Organ: root; Vector: pBluescriptII SK+; Site 1:
ECORI; Site 2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"

FEATURES

source

ORIGIN

Query Match	60.1%; Score 652.4; DB 2; Length 668;
Best Local Similarity	99.8%; Pred. No. 1.1e-171;
Matches	653; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	397 ACTGTGCTGCTACTATTGAGGCAAGGAGGATTTCAAAATATGGAGAATACACCACCA 456
Db	14 ACTGTGCTGCTACTATTGAGGCAAGGAGGATTTCAAAATATGGAGAATACACCACCA 73
Qy	457 GTGATAGAACCCCCACAGCAAAACCAAATACAGCATGACTACTACACAGTGCCACACGAA 516
Db	74 GTGATAGAACCCCCACAGCAAAACCAAATACAGGCATGACTACTACAACTGTCACACGAA 133
Qy	517 GTGCTACTGACAAATATTTGCTAAAGGGTGTTCCTGCTGATAGTGTAGTCAATTGTTGGT 576
Db	134 GTGGTACTGCAATATTTGCTAAAGGGTGTTCCTGCTGATAGTGTAGTCAATTGTTGGT 193
Qy	577 GAAACAGATGTTGATGATATCCATTGAAGTTCCTGGTGAAGAACCATACCAATTTTCAGCCC 636
Db	194 GAAACAGATGTTGATGATATCCATTGAAGTTCCTGGTGAAGAACCATACCAATTTTCAGCCC 253
Qy	637 CGTCTGTTTTCTAAGATTTATCCCTGAGAAATGCAAAATATCAAGTCTTTATCCACCAAGGTT 696
Db	254 CGTCTGTTTTCTAAGATTTATCCCTGAGAAATGCAAAATATCAAGTCTTTATCCACCAAGGTC 313
Qy	697 GAAATACGCTTTCGAAAAGCTGACGAGGTTGACATGGACACCCCTGGATTTATAGTGGAGA 756
Db	314 GAAATACGCTTTCGAAAAGCTGACGAGGTTGACATGGACACCCCTGGATTTATAGTGGAGA 373
Qy	757 CCAAGACGTGTTCCCCAGAGAAGATAAGCAGCGCCAGCTGAAACACAGCCCCCAAGACCTTTCATAC 816

RESULT 4
CD443320
LOCUS

Department of Biological Sciences

752 bp
mRNA linear EST 03-JUN-2003

DEFINITION ELO1N042G10.b Endosperm_4 Zea mays cDNA, mRNA sequence.

ACCESSION CD443320

VERSION CD443320.1 GI:31358963

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 752)

Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,

Larkins, B., Becraft, P. and Messing, J.

Characterization of the maize endosperm transcriptome and its

comparison to the rice genome

Genome Res. 14 (10), 1932-1937 (2004)

Contact: Lai, Jinheng

Dr. Joachim Messing's lab

Wakeman Institute, Rutgers University

190 Frelinghuysen Rd., Piscataway, NJ 08854, USA

Tel: 732-445-3801

Fax: 732-445-5735

Email: jlai@wakeman.rutgers.edu

Seq primer: T3.

Location/Qualifiers

1..752

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="W22"

/db_xref="taxon:4577"

/tissue_type="Endosperm of 7-23DAP"

/clone_lib="Endosperm_4"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI"

ORIGIN

Query Match 59.9%; Score 650.2; DB 6; Length 752;
 Best Local Similarity 99.5%; Pred. No. 4.9e-171;
 Matches 652; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCCCGCTCGGATCTGGAGCAAGGCCAAGGAGGCTTCGTCGAGCAGCTTCGAG 60
 Db 98 ATGCCCGCTCGGATCTGGAGCAAGGCCAAGGAGGCTTCGTCGAGCAGCTTCGAG 157

Qy 61 CTGCCACCGAGCTCTACAGCCAGGCCATCGACGCCGGGCCGCCACCGCGAGCTCTAT 120
 Db 158 CTGCCACCGAGCTCTACAGCCAGGCCATCGACGCCGGGCCGCCACCGCGAGCTCTAT 217

Qy 121 GCCACCGCGCCGCGCCACATCAAGCTCGGCACTACACTGAGGCTGTGGCGGATGCT 180
 Db 218 GCCACCGCGCCGCGCCACATCAAGCTCGGCACTACACTGAGGCTGTGGCGGATGCT 277

Qy 181 AACAAAGCAATGAGCTTGATCTTATGATGATTAAGCTTACTACCGAAGGCTGCTGCA 240
 Db 278 AACAAAGCAATGAGCTTGATCTTATGATGATTAAGCTTACTACCGAAGGCTGCTGCA 337

Qy 241 TGCATTAAAGCTTGAAGATAACAACTGCAAGGCTGCTTTGAGTTGGGTTCTTCTAT 300
 Db 338 TGCATTAAAGCTTGAAGATAACAACTGCAAGGCTGCTTTGAGTTGGGTTCTTCTAT 397

Qy 301 GCATCAGCGAATTCAGGTTTGTCTCTATTAAGGATGATGAGCGCATCGCTGAG 360
 Db 398 GCATCAGCGAATTCAGGTTTGTCTCTATTAAGGATGATGAGCGCATCGCTGAG 457

Qy 361 GAATCTAGCAGGACCAAGTAAGATGTTGAGGCTACTGTGGCTGCTACTATTGAGGAC 420
 Db 458 GAATCTAGCAGGACCAAGTAAGATGTTGAGGCTACTGTGGCTGCTACTATTGAGGAC 517

Qy 421 AAGGAGGATTTACAAATATGGAGATAACACACAGTGTAGAACCCGCCCAAGCAACCA 480
 Db 518 AAGGAGGATTTACAAATATGGAGATAACACACAGTGTAGAACCCGCCCAAGCAACCA 577

Qy 481 AATACAGGCAATGACTACTACACAGTCCACAGAGTGGTACTGACATATTTGCTAAG 540

Db 578 AATACAGGCAATGACTACTACACAGTCCACAGAGTGGTACTGACATATTTGCTAAG 637
 Qy 541 GGTGTTCTCTCTGATAGTGTAGTCAATGATTTTGGTGAACAGAGTGTGAGTATCCATT 600
 Db 638 GGTGTTCTCTCTGATAGTGTAGTCAATGATTTTGGTGAACAGAGTGTGAGTATCCATT 697

Qy 601 GAGTTTCTCTGTTGAAGAACCATACATTTTCAGCCCGCTCTGTTTCTAGATTA 655
 Db 698 GAGTTTCTCTGTTGAAGAACCATACATTTTCAGCCCGCTCTGTTTCTAGATTA 752

RESULT 5

CA184150

LOCUS

DEFINITION

CA184150

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

complex.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 756)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda, P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Pax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: 142 row: H column: 05

Seq primer: T7 promoter Primer.

Location/Qualifiers

1..756

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCRPT3142H05"

/lab_host="DH10B"

/clone_lib="ST3"

/notes="Organ: Fourth apical stalk internodes of adult

plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An

unidirectional cDNA library generated from [Fourth apical

stalk internodes of adult plants]. cDNA was prepared from

polyA+ mRNA using SuperScript Plasmid System Kit

(Invitrogen). The double-strand cDNAs were fractionated

in a sepharose CL-2B 40cm-columns and fragments sizing

between 0.8 and 1.5 Kb were directionally cloned into the

vector. Details of each source of RNA and library

construction can be obtained at

http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 59.6%; Score 647; DB 6; Length 756;
 Best Local Similarity 95.0%; Pred. No. 3.9e-170;
 Matches 721; Conservative 0; Mismatches 32; Indels 6; Gaps 5;

Qy 4 GCCCGCTCGGATCTGAGAGCAAGGCCAAGGAGGCTTCGTCGAGCAGCTTCGAGCTG 63
 Db 3 GCCCGCTCGGATCTGAGAGCAAGGCCAAGGAGGCTTCGTCGAGCAGCTTCGAGCTG 62

Qy 64 GCCACCGAGCTCTACAGCCAGGCGCATCGACGCCGGGCCGCCACCGCGGACCTCTAGCC 123
 Db 63 GCCCGCGAG--CTACACCCAGGCGCATCGACGCCGGGCCGCCACCGCGGACCTCTAGCC 120

124	Qy	GACCGGCCAGGCGCACATCAAGCTCGGCAACTACACTGAGGCTGTGGCGGATGCTTAAC	183
121	Db	GACCGGCCAGGCGCACATCAAGCTCGGCAACTACACTGAGGCTGTGGCGGATGCTTAAC	180
184	Qy	AAAGCAATTGAGCTTGATCTTATGATGATCAAAAGCTTACTACCGGAAAGGTGCTGCATGC	243
181	Db	AAAGCAATTGAGCTTGATCTTATGATGATCAAAAGCTTACTACCGGAAAGGTGCTGCATGC	240
244	Qy	ATTAAGCTTTGAAGAATACCAAACTGCAAGGCTGCTCTTGAGTTGGGTCTCTTTATGCA	303
241	Db	ATTAAGCTTTGAAGAATACCAAACTGCAAGGCTGCTCTTGAGTTGGGTCTCTTTATGCA	300
304	Qy	TCAGGCGATTCAAGGTTTCTGCTCTATTGAAGGAATGTGATGAGCGCATCGCTGAGAA	363
301	Db	TCAGGCGATTCAAGGTTTCTGCTCTATTGAAGGAATGTGATGAGCGCATCGCTGAGAA	360
364	Qy	TCTAGCCAGGCAAGCAAGTAAGGCTTCTG	

source

1. 659

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W23"
/db_xref="taxon:4577"
/tissue_type="root"
/dev_stage="3-4 days old"
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/clone_lib="614 - root cDNA library from Walbot Lab"
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ORIGIN

Query Match		59.2%; Score 643.4; DB 2; Length 659;
Best Local Similarity		99.8%; Pred. No. 3.8e-169;
Matches 644; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	240	ATGCATTAAAGCTTGAAGAAATACCAAACTGCAAGGCTGCTCTTGAGTTGGGTCTCTCTTA 299
Db	15	ATGCATTAAAGCTTGAAGAAATACCAAACTGCAAGGCTGCTCTTGAGTTGGGTCTCTCTTA 74
Qy	300	TGCATCAGGCGATTCAGAGTTTGCCTCTATTGAAGGAATGTGATGAGCGCATCGCTGA 359
Db	75	TGCATCAGGCGATTCAGAGTTTGCCTCTATTGAAGGAATGTGATGAGCGCATCGCTGA 134
Qy	360	GGAATCTAGCCAGGCAAGTAAAGAAATGTGAGGCTACTGTGGCTGCTACTATTGAGGA 419
Db	135	GGAATCTAGCCAGGCAAGTAAAGAAATGTGAGGCTACTGTGGCTGCTACTATTGAGGA 194
Qy	420	CAAGGAGGATTCACAAATATGGAATACACCAAGCTGATAGAACCCCAAGCAAAACC 479
Db	195	CAAGGAGGATTCACAAATATGGAATACACCAAGCTGATAGAACCCCAAGCAAAACC 254
Qy	480	AAATACAGGCGATGACTACTACACAGTGCACAGAGTGGTACTGACAAATATTGCTAA 539
Db	255	AAATACAGGCGATGACTACTACACAGTGCACAGAGTGGTACTGACAAATATTGCTAA 314
Qy	540	GGGTGTTCTGCTGATAGTGTAGTCATTGATTTTGGTGAACAGATGTTGAGTATCCAT 599
Db	315	GGGTGTTCTGCTGATAGTGTAGTCATTGATTTTGGTGAACAGATGTTGAGTATCCAT 374
Qy	600	TGAAGTTCTGCTGATGAAGAACCATACATTTCAGCCCGCTGTTTCTAGATTTATCCC 659
Db	375	TGAAGTTCTGCTGATGAAGAACCATACATTTCAGCCCGCTGTTTCTAGATTTATCCC 434
Qy	660	TGAGAAATGCAAAATATCAAGTCTTATCCCAAGGTTGAAATACGCTTGCAAAAGCTGA 719
Db	435	TGAGAAATGCAAAATATCAAGTCTTATCCCAAGGTTGAAATACGCTTGCAAAAGCTGA 494
Qy	720	GCAGGTGACATGGGCAACCCCTGGATTATAGTGGAGAACCAAGACTGTTCCCGAGAGAT 779
Db	495	GCAGGTGACATGGGCAACCCCTGGATTATAGTGGAGAACCAAGACTGTTCCCGAGAGAT 554
Qy	780	AAGCAGCCGAGCTGAAGACCCCAAGACCTTCATACCCCTCTTCAAGGCGGAAAAAGA 839
Db	555	AAGCAGCCGAGCTGAAGACCCCAAGACCTTCATACCCCTCTTCAAGGCGGAAAAAGA 614
Qy	840	CTGGGATAAACTGGAAGCTGAAGTCAAAAAGGAGGAGAGGAAGA 884
Db	615	CTGGGATAAACTGGAAGCTGAAGTCAAAAAGGAGGAGAGGAAGA 659

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: April 23, 2005, 00:00:36 ; Search time 5229.64 Seconds
(without alignment)
10590.311 Million cell updates/sec

Title: US-10-609-078-7
Perfect score: 1455
Sequence: 1 gaattggcagcgccgac.....aaaaaaaaaaaaaaaaaaaa 1455

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gsel:*
- 9: gb_gsel2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1378.2	94.7	1646	3	AY103953	AY103953 Zea mays
2	719	49.4	727	6	CA401716	CA401716 EL01N0424
3	708.2	48.7	752	6	CD443320	CD443320 EL01N0424
4	699	48.0	1131	9	CL959360	CL959360 O8IFCC002
5	660.6	45.4	686	6	CF041238	CF041238 QIC23f02.
6	657.2	45.2	772	6	CA258233	CA258233 SCCCT300
7	652.4	44.8	668	2	AW076274	AW076274 614063D11
8	650.8	44.7	798	6	CA176210	CA176210 SCJLST102
9	647	44.5	756	6	CA184150	CA184150 SCRFST314
10	643.4	44.2	659	2	AW090936	AW090936 614068G07
11	641	44.1	759	6	CA245820	CA245820 SCEZFL508
12	637.4	43.8	778	6	CA227695	CA227695 SCJLFL301
13	631	43.4	666	6	CA215140	CA215140 SCSBAD112
14	628.8	43.2	681	2	AW076372	AW076372 614066C10
15	627	43.1	658	2	AW155786	AW155786 614096F11
16	623.2	42.8	648	1	AI603781	AI603781 486096G09
17	615.4	42.3	665	6	CA153735	CA153735 SCVPRZ203
18	608.2	41.8	678	6	CA177070	CA177070 SCWCST105
19	601.8	41.4	725	6	CA094787	CA094787 SCCCL401
20	601	41.3	609	7	CK826852	CK826852 zmrsub1.0
21	600.2	41.3	609	2	AW017784	AW017784 614063D11
22	599.4	41.2	640	6	CF002911	CF002911 QBH17D05.
23	596.4	41.0	622	6	CA229980	CA229980 SCJFL3C0
24	595.8	40.9	599	2	AW331768	AW331768 614096F11

25	594.8	40.9	730	2	BE362001	BE362001 DG1 83 HO
26	591	40.6	591	2	AW018202	AW018202 614068G07
27	589.8	40.5	593	4	BG265701	BG265701 1000034P0
28	584.4	40.2	594	1	AI601072	AI601072 486096G09
29	583.4	40.1	586	2	AW042392	AW042392 614028B03
30	583.4	40.1	609	6	CA229238	CA229238 SCAGFL302
31	579.8	39.8	718	6	CA106435	CA106435 SCQHR101
32	576.8	39.6	702	6	CA282995	CA282995 SCPLB202
33	576	39.6	588	5	BU499669	BU499669 946178B11
34	571.2	39.3	680	6	CA128103	CA128103 SCAGL203
35	567.8	39.0	578	2	AW000264	AW000264 614009H02
36	565.2	38.8	594	6	CA098274	CA098274 SCMCCL605
37	563	38.7	574	4	BI644145	BI644145 949022C08
38	560.6	38.5	914	6	CA084222	CA084222 SCFQAM203
39	560.4	38.5	579	2	AW054458	AW054458 660007D01
40	560.2	38.5	607	1	AI601071	AI601071 486096G09
41	558.4	38.4	560	2	AW018065	AW018065 614066C10
42	557.2	38.3	630	6	CA486265	CA486265 WHB4329.D
43	556.4	38.2	578	6	CD996630	CD996630 QBC6a07.X
44	555.6	38.2	579	2	AW066518	AW066518 660015G08
45	555.6	38.2	736	6	CA227777	CA227777 SCJLFL301

ALIGNMENTS

RESULT 1
AY103953
LOCUS Zea mays PC0098564 mRNA sequence. 1646 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PC0098564 mRNA sequence.
ACCESSION AY103953
VERSION AY103953.1 GI:21207031
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 1646)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1646)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES
Location/Qualifiers
1..1646
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:635643"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 94.7% Score 1378.2; DB 3; Length 1646;

	Best Local Similarity	98.7%;	Pred. No. 0;	Mismatches	18;	Indels	0;	Gaps	0;	
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Qy	24	AGTCATCGTCTGCTCGTCCGCGCAGAGCGCGACGCCCAAAGCGGAAGGGCGGCAT	83							
Dd	143	AGTCATCGTCTGCTCGTCCGCGCAGAGCGCGACGCCCAAAGCGGAAGGGCGGCAT	202							
Qy	84	GGCGCGTCCGATCTGGAGAGCAAGGCCAAGAGGCGCTTCGTGCGACGACGACTTCGAGCT	143							
Dd	203	GGCGCGTCCGATCTGGAGAGCAAGGCCAAGAGGCGCTTCGTGCGACGACGACTTCGAGCT	262							
Qy	144	GGCCACCGAGCTCTACAGCCAGGCCCATCGACCGCGGCCCGCCACCGCCGACCTCTATGC	203							
Dd	263	GGCCACCGAGCTCTACAGCCAGGCCCATCGACCGCGGCCCGCCACCGCCGACCTCTATGC	322							
Qy	204	CGACCGCGCCACAGGCGCACATCAAGCTCGGCAACTACACTGAGGCTGTGGCGGATGCTAA	263							
Dd	323	CGACCGCGCCACAGGCGCACATCAAGCTCGGCAACTACACTGAGGCTGTGGCGGATGCTAA	382							
Qy	264	CMAAGCAATTGAGCTTGATCTCTATGATGATATAAGCTTTACTACCGAAAAGGTGCTGCATG	323							
Dd	383	CMAAGCAATTGAGCTTGATCTCTATGATGATATAAGCTTTACTACCGAAAAGGTGCTGCATG	442							
Qy	324	CATTAAAGCTTGAAGAATACCAAACTGCAAGGCTGCTCTTGAGTTGGGTTCTCTTATGC	383							
Dd	443	CATTAAAGCTTGAAGAATACCAAACTGCAAGGCTGCTCTTGAGTTGGGTTCTCTTATGC	502							
Qy	384	ATCAGGCAATCAAGGTTTGCTGCTCTATTGAAGGAATGTGATGAGCGCATCGCTGAGGA	443							
Dd	503	ATCAGGCAATCAAGGTTTGCTGCTCTATTGAAGGAATGTGATGAGCGCATCGCTGAGGA	562							
Qy	444	ATCTAGCCAGGCACAGTAAGAATGTTGAGGCTACTGTGCTGCTACTATTGAGGACAA	503							
Dd	563	ATCTAGCCAGGCACAGTAAGAATGTTGAGGCTACTGTGCTGCTACTATTGAGGACAA	622							
Qy	504	GGAGGATTTCAAAATATGAGAGATACACCAGTAGTATGAAACCCCAAGCAAAACCAA	563							
Dd	623	GGAGGATTTCAAAATATGAGAGATACACCAGTAGTATGAAACCCCAAGCAAAACCAA	682							
Qy	564	ATACAGGATGACTACTACAACAGTGCCACAGAGTGATCTGACATATTTGCTTAAGG	623							
Dd	683	ATACAGGATGACTACTACAACAGTGCCACAGAGTGATCTGACATATTTGCTTAAGG	742							
Qy	624	TGTTCTGCTGATAGTGAGTCAITGATTTTTGGTGAACAGATGTTGAGTGATCCATTGA	683							
Dd	743	TGTTCTGCTGATAGTGAGTCAITGATTTTTGGTGAACAGATGTTGAGTGATCCATTGA	802							
Qy	684	AGTTCTCGTGAAGAACATACCATTTACGCCCGGCTGTTTCTTAAGATATTCCTGTA	743							
Dd	803	AGTTCTCGTGAAGAACATACCATTTACGCCCGGCTGTTTCTTAAGATATTCCTGTA	862							
Qy	744	GAATATGCAATATCAAGTCTTTATCCACCAAGTTGAAATACGCTTCGAAAGCTGAGCA	803							
Dd	863	GAATATGCAATATCAAGTCTTTATCCACCAAGTTGAAATACGCTTCGAAAGCTGAGCA	922							
Qy	804	GGTGACATGGAACACCTGGATTATAGTGGAGAACCAAGACTGTTCCCAGAGATAAG	863							
Dd	923	GGTGACATGGAACACCTGGATTATAGTGGAGAACCAAGACTGTTCCCAGAGATAAG	982							
Qy	864	CACGCCAGCTGAAACAGCCCCAGACCTTCATACCCATCTTCAAGCGGAAAAAGACTG	923							
Dd	983	CACGCCAGCTGAAACAGCCCCAGACCTTCATACCCATCTTCAAGCTCAAAAAAGACTG	1042							
Qy	924	GGATATAACTGGAAGCTGAAGTCAAAAAAGGAGGAGAGAGAAACCTTCGATGCTGATGC	983							
Dd	1043	GGATATAACTGGAAGCTGAAGTCAAAAAAGGAGGAGAGAGAAACCTTCGATGCTGATGC	1102							
Qy	984	TGCATTGAAACAAATTTCTCGTGATCTACAGGATGCTGATGAAGATATGCGAGGGC	1043							
Dd	1103	TGCATTGAAACAAATTTCTCGTGATCTACAGGATGCTGATGAAGATATGCGAGGGC	1162							
Qy	1044	CATGATGAAGTCATTCTGTGAATCAAAATGGCAGTGTCTCTCAACCAATTTGGAAGATGT	1103							

Db	1163	CATGATGAAGTCATCTCGTGGGAATCAAAATGGCAGCTGTGTTCTCTCTCAACCAATTTGGAAAGATGT	1222
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Db	1223	TGGAGCAAAAGAGGTAGAGGGAGGAGCCCTCTGATGGTATGAGAGCTCAAGAGTGGGAATA	1282
QY <td>1164</td> <td>CTAAAGTTTGGACTGCCCGTCTTTTGTAAATCCAGGTCCTTGGAAAACTATGACCTAAATTC</td> <td>1223</td>	1164	CTAAAGTTTGGACTGCCCGTCTTTTGTAAATCCAGGTCCTTGGAAAACTATGACCTAAATTC	1223
Db	1283	CTAAAGTTTGGACTGCCCGTCTTTTGTAAATCCAGGTCCTTGGAAAACTATGACCTAAATTC	1342
QY <td>1224</td> <td>GCCACCCATAGTGCATGAGCTGCTTGGTAAAGTCTCTGCTTTGTAAAGCTTTCTGTA</td> <td>1283</td>	1224	GCCACCCATAGTGCATGAGCTGCTTGGTAAAGTCTCTGCTTTGTAAAGCTTTCTGTA	1283
Db	1343	GTCACCCATAGTGCATGAGCTGCTTGGTAAAGTCTCTGCTTTGTAAAGCTTTCTGTA	1402
QY <td>1284</td> <td>TGACAGTCTAGCGTGTCTGAGTGCTACTTGGCGTAGCTTTTGAATGGACATAGGTATGC</td> <td>1343</td>	1284	TGACAGTCTAGCGTGTCTGAGTGCTACTTGGCGTAGCTTTTGAATGGACATAGGTATGC	1343
Db	1403	TGACAGTCTAGCGTGTCTGAGTGCTACTTGGCGTAGCTTTTGAATGGACATAGGTATGC	1462
QY <td>1344</td> <td>TATTATGTGTATCGACCCGACCAATCTGTGTATCAAGACAGCAAACTATAATGTAT</td> <td>1403</td>	1344	TATTATGTGTATCGACCCGACCAATCTGTGTATCAAGACAGCAAACTATAATGTAT	1403
Db	1463	TATTATGTGTATCGACCCGACCAATCTGTGTATCAAGACAGCAAACTATAATGTAT	1522
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DEFINITION	E01N0424G10.g Endosperm_4 Zea mays cDNA, mRNA sequence.		
ACCESSION	CA401716		
VERSION	CA401716.1		
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	Lai, J., DeV, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Becraft, P. and Messing, J.		
TITLE	Characterization of the maize endosperm transcriptome and its comparison to the rice genome		
JOURNAL	Genome Res. 14 (10), 1932-1937 (2004)		
COMMENT	Contact: Lai, Jinsheng Dr. Joachim Messing's lab Waksman Institute, Rutgers University 130 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801 Fax: 732-445-5735 Email: jlai@waksman.rutgers.edu Seq primer: T7		
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Qy	712	CAGCCCCGCTGTTTTCTAAAGATTATCCCTGAGAAATGCAAAATATCAAGTCTTATCCACC	771		
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Page 3

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1018	QY	GATGCTGATGAAGATATCCGGAGGCGCCATGATGAAGTCAITTCGTGGATCAATCGCACT	1077
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RESULT	8
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	3', mRNA sequence.
ACCESSION	CAL76210
VERSION	CAL76210.1 GI:35105709
KEYWORDS	EST.
SOURCE	Saccharum officinarum
ORGANISM	Saccharum officinarum
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	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
	clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
	complex.
REFERENCE	1 (bases 1 to 798) Kerner E.L. and Artuda P.

REFERENCE
1 (bases 1 to 798)
complex.
Kerner, E. L., and Arruda, P.

AUTHORS	Vettore, A.L., da Silva, F.R., Rempel, L.
TITLE	The libraries that made SUCEST
ISSN	0013-798X
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JOURNAL
Genet. Mol. Biol. 24 (1-2), 1-2 (2001)
COMMENT
Contact: Arruda P

COMISSÃO:
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Instituto de Física, Estadual de Campinas

Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089
Email: parruda@unicamp.br

clone distribution: clone distribution information

through the Brazilian Clone Collection Center
<http://www.bcccenter.fcav.unesp.br>

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PREFERENCE	1 (bases 1 to 668)							

Unpublished (1999)	University	Walbot V	Stanford University	855 California Ave, Palo Alto, CA 94304, USA	850 723 2227	650 725 8221	walbot@stanford.edu	11.
CONTACT	JOURNAL	source	FEATURES	Location/Qualifiers	Plate: 614063	row: D	column: 11.	1. .668

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